

SEQUENCE LISTING



<110> Gordon, Lynn K.
 Goodglick, Lee
 Goldman, Melissa

<120> NOVEL GENES AND POLYPEPTIDES FOR THE
 DIAGNOSIS OF GIANT CELL ARTERITIS

<130> 07419-029001

<140> 09/484,577

<141> 2000-01-18

<160> 98

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 682

<212> DNA

<213> Homosapiens

<220>

<223> artificially generated nucleic acid

<400> 1

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gacaggctcg	ctgccctcct	cgcgcaagtt	ctttgcaatc	cctgaggccg	cgcccgacat	180
ccgcgttccc	ttgcgcgaga	tcctcctgtc	cgagggcgcc	ggcgagccga	acctgccggt	240
ctatgacacc	tcggggccct	acaccgatcc	ggccgtgacg	atcgacgtca	acagcggcct	300
gccgcgcaat	cgctctgcct	gggtcaagga	acgcggcggc	gtcgaggaat	atcaggccgc	360
accatcaagc	cggaggacaa	cggcaatgtc	ggcgcacccc	acgccgcaa	ggcggttcacc	420
ggcaccacaa	gccgctgcgc	ggctcgacgg	cacaagatca	cccactcgag	ttcgccgcgc	480
cggcattata	ccaaggagat	gatctacgtc	gccgagcgtg	agaatcttgg	cgcaagcagc	540
agctgagcgc	gccgaggccg	gctgccgacg	gaagagtttt	ggcgccgcgg	tgccggctta	600
ttacgccgga	atttgtcgca	agagatcgcg	cggcgggccat	tatttccttt	aaaattaaca	660
ttgccgagct	tgaaccgatg	aa				682

<210> 2

<211> 92

<212> PRT

<213> Homosapiens

<400> 2

Leu	Pro	Ala	Val	Thr	Gly	Ser	Leu	Pro	Ser	Ser	Arg	Lys	Phe	Phe
1				5				10					15	
Ala	Ile	Pro	Glu	Ala	Ala	Pro	Asp	Ile	Arg	Val	Pro	Leu	Arg	Glu
		20						25				30		
Ile	Leu	Ser	Glu	Gly	Ala	Gly	Glu	Pro	Asn	Leu	Pro	Val	Tyr	Asp
		35					40					45		
Ser	Gly	Pro	Tyr	Thr	Asp	Pro	Ala	Val	Thr	Ile	Asp	Val	Asn	Ser
		50				55					60			
Leu	Pro	Arg	Asn	Arg	Leu	Ala	Trp	Val	Lys	Glu	Arg	Gly	Gly	Val
65					70				75					80
Glu	Tyr	Gln	Ala	Ala	Pro	Ser	Ser	Arg	Arg	Thr	Thr			
				85					90					

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<210> 3
 <211> 501
 <212> DNA
 <213> Homosapiens

<220>
 <223> Synthetically generated nucleic acid

<400> 3
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 aaccgggac gagctggcct tctgcccgc cgcctcgaa attgtcgaga cgccgccatc 120
 tcccaccgcg agactcacgg ccgccttgct tgctgccttg ttctactgcg ccgtggcggtg 180
 ggcggtgtctc ggcaggatcg acatcgttgc ttctgcatcc agaaagatcg tgcggggcga 240
 ccgtgtaaag ctggttcagc cgctcgaggt cggcgtggtg cgggccactc atgtccgcga 300
 tggccaaacc gtcaaggccg gcgagattct gatcgagctg gatccattcg cgggtggtgt 360
 ggatgttgcg ccccgtcaga ggtccatcac ggtgtcggcg cccacggat cgccacacca 420
 tctgtcgac ctttcttcac cgacgagtca ccgccgagtt gccgatattg cgtgatctta 480
 tcagaatgcg gcgatgatca t 501

<210> 4
 <211> 124
 <212> PRT
 <213> Homosapiens

<400> 4
 Leu Ser Ser Leu Ser Pro Arg Met Lys Ser Ala Arg Glu Val Val Ala
 1 5 10 15
 Val Gly Gly Lys Thr Arg Asp Glu Leu Ala Phe Leu Pro Ala Ala Leu
 20 25 30
 Glu Ile Val Glu Thr Pro Pro Ser Pro Thr Ala Arg Leu Thr Ala Ala
 35 40 45
 Leu Leu Ala Ala Leu Phe Tyr Cys Ala Val Ala Trp Ala Gly Leu Gly
 50 55 60
 Arg Ile Asp Ile Val Ala Ser Ala Ser Arg Lys Ile Val Pro Gly Asp
 65 70 75 80
 Arg Val Lys Leu Val Gln Pro Leu Glu Val Gly Val Val Arg Ala Thr
 85 90 95
 His Val Arg Asp Gly Gln Thr Val Lys Ala Gly Glu Ile Leu Ile Glu
 100 105 110
 Leu Asp Pro Phe Ala Gly Gly Val Asp Val Ala Thr
 115 120

<210> 5
 <211> 747
 <212> DNA
 <213> Homosapiens

<220>
 <223> Artificially generated nucleic acid

<400> 5
 accgacgtcg actatccatg aacggatccc tgcaacgaca tcgtgcgtac ggcctatgaa 60
 gcgctcgccg ccgtgctcgg tggcacgcag tcgctccaca ccaactcgtt cgacgaggcg 120
 atcgcgctgc cgattgactt ctccgcccgg atcgcccgcga acaccagctg atccagcagc 180
 acgagacaga cgtcacggac gcggtcgaca ctctggcggg gtcctactac gtggagcgcc 240
 tgacggatga cctcgccaag cgggcctggg agctgatgga agaggtcgag aagatgggtg 300
 gcatggcgca ggcgatcgcg accggttggc cgaagcgctt gatcgagcaa tctgcgacgc 360
 aaaagcaggc cgcgatcgat cgcggcgatc aggtgatcgt gggcgtgaac cgctaccggc 420
 ccgaacagga gcaaccgatc gacattattg agatcgacaa ctcgacgggtt cgggcctccc 480
 agatccggtg tctcgccgaa atcgaaaagg cgcgtgattc aaggaagggt gagtccgcgc 540
 tcgggggagct ggcgtgtatt gcccgcacgg gtgagggaaa tctgctggct gcagcgaccg 600

```

agcccgctcg cgcgcgggct accgtcggg agatgtccga cgccatgcgg caagcattcg 660
gcgaccacga ggcggtgccg gaggtagtgt cggacgttta cggccgtgcc tatggcacgg 720
atccgttcac ggatagtcga cgtcgggt 747

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<210> 6
<211> 48
<212> PRT
<213> Homosapiens

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<400> 6
Asp Pro Cys Asn Asp Ile Val Arg Thr Ala Tyr Glu Ala Leu Ala Ala
 1           5           10           15
Val Leu Gly Gly Thr Gln Ser Leu His Thr Asn Ser Phe Asp Glu Ala
      20           25           30
Ile Ala Leu Pro Ile Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Ser
    35           40           45

```

```

<210> 7
<211> 301
<212> DNA
<213> Homosapiens

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<220>
<223> Synthetically generated nucleic acid

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<400> 7
actctccagc ctctcaccga ggatcatcga cgacattaag cagctggccg acaacggcgt 60
gcgcggaattc acgctgatcg gacagaatgt caacgcctac cacggcggag ggcccgcgag 120
ccgcgtctgga ccgctcggca aattgctgca gcgactcgcg gacattccag gcgtcatgcg 180
gctgcgttat tcgatcagcc atccgcgcga cgtcgacgac agcctgatcg ccgcgcacg 240
cgatttgccc ggactgatgc cgttcgtgca cctgccggtg caatcggggg cggaccggat 300
c 301

```

```

<210> 8
<211> 91
<212> PRT
<213> Homosapiens

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```

<400> 8
Ile Ile Asp Asp Ile Lys Gln Leu Ala Asp Asn Gly Val Arg Glu Phe
 1           5           10           15
Thr Leu Ile Gly Gln Asn Val Asn Ala Tyr His Gly Gly Gly Pro Asp
      20           25           30
Gly Arg Val Trp Pro Leu Gly Lys Leu Leu Gln Arg Leu Ala Asp Ile
    35           40           45
Pro Gly Val Met Arg Leu Arg Tyr Ser Ile Ser His Pro Arg Asp Val
    50           55           60
Asp Asp Ser Leu Ile Ala Ala His Arg Asp Leu Pro Gly Leu Met Pro
65           70           75           80
Phe Val His Leu Pro Val Gln Ser Gly Ala Asp
      85           90

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```

<210> 9
<211> 620
<212> DNA
<213> Homosapiens

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<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

```

```

<400> 9
actctccanc ctctcaccga ggatcagaat aggtgaagag cgaagacacc gagaacgtct 60
ggccttgaac ggacagcgtg cttgagttgg tcgggggtcac caccggaccc gtgtccaccg 120
gcgcagtcac ngtgaaagca cttgaccatg atcccagacg gtgccgtcat ccgcgcggac 180
ccacancgtn tccgcgcccc accggattga tagctcagcg acaccagctg ggctgccgtg 240
acgtanttgt gctggttngg tgcaagtgcc accccgctca agacaaantg gccgcacctg 300
tgcccgtgtc ccaaactgca tattgggtcg cagcactgtc gaacggatca ctgtangtgc 360
acagcgacna anccgcatan ctctngccgt ggggcgcaac gatgttnnac accgtctcaa 420
cggttaccgt gtcnagggga ncatttacng ggaaagcatt cgaccactcc cccacaccgt 480
gcccgcattt gcgcggattc ctttcattga tatgtccacg tcggtnggnc tttaagcngg 540
cggcaaccgc ggtgnagctn cactttttgt tccttttatt ganggttaat ttgcgcgctt 600
tggnctgaan tntttngaan 620

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<210> 10
<211> 662
<212> DNA
<213> Homosapiens

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<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

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<400> 10
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ctgggtatth cagcgaaccg ctctgcgctt ggcgggaaac accgacgcgc ttgaaggctt 120
accggacgac acgcgcgcag ccttgattcg aatgcactctg gagtacttgc gcagtcagga 180
ttccgagcag cgcgccaagc tgtccgaact ggatcagcaa cgggtgcaga aggtcgcgga 240
gaccaggacg atcgacgcca gcatcgcgaa gattgaagct ttgctgcggt gctgcaggan 300
cggttcgggg ttcgcaagta cctggcggac agggagtacg gctcaaagct gcaatattcg 360
caggaactcc aggaactggt cgggatgcag caggacatcc tgggtgcaac gagcaaagct 420
cgaggaaacc aatgcggntt gtcgcccacg ttcgacgaaa acccgcgna agcttcgtct 480
nngaataacc ggcacccgnc tgttccnacc atcttgcccc aaggggacgc aaaaaagggc 540
cggcaagncc tcaaaggacc aaggngttt taaaanccga gcacccggga cccaaccttt 600
aaaaancntt ggcggccccc attcgacggn gtggnngcaa caaattgggc cngccccat 660
tt 662

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<210> 11
<211> 242
<212> DNA
<213> Homosapiens

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<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

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<400> 11
actctcnngc ctctcaccga agatagccgg caaggactgg cngaacann gcgcgctgga 60
ctatcnctaa aggttctccn acnacgtcca nccggacnag ctgacctcgt ttccnnaag 120
cgtgaaactg aaggccggtg aaacctent gttcgcttng atcacctact agtcgcgcgc 180
cnngcgcgac aggatcaacg ccaagggtgat ggccgatccc cgcttggcgt cgtcgatgga 240
tc 242

```

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<210> 12
<211> 552
<212> DNA
<213> Homosapiens

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<400> 12

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gatccgctcg	atgcccaggc	ccagtacagc	gaactgttcg	cccatggccg	cgccacgtca	60
ctgttgctat	tccaacatgt	tcacggtgaa	tcccgtagcc	gcggccaggc	gatggtggac	120
ctgctggcgc	agtacgagca	gcacggtttg	cagttaaaca	gccgcgaatt	accggaccac	180
ctgccgctgt	atctggagta	cctgtcgcag	ctgccgcaag	gcgaagccgt	ggaaggtttg	240
aaagatatcg	cgccgattct	ggcattgctg	agcgcgcgct	tgcaacagcg	tgaaagccgt	300
tatgccgtga	tgtttgatct	gctgctgaaa	ttggccgata	ccgctatcga	cagcgacaaa	360
gtggcgga	aaattgccga	cgaagcgcg	gatgatacgc	cgcaggcgct	ggatgctgtt	420
tggaagaag	agcagggtta	attcttttgc	gacaaaggct	gcggcgattc	agcaatcact	480
gctcatcagc	gtcgctttgc	cggtgccgct	gcggcgcaat	atctgaatat	cctcggtgag	540
aggctggaga	gt					552

<210> 13

<211> 265

<212> DNA

<213> Homosapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> N=A,T,C or G

<400> 13

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ggcgggtnaa	agtgaacatc	cgccgagcac	ggcagcgacg	cctccgctca	ccgtcngcgc	120
agtacttcct	cgggctgcgc	cgcctagcac	tctgcgccgt	gacatcaanc	cgtgaaccga	180
cgggagactt	tgcgccgcna	agggatgagt	ccactattag	atgacgcatg	gctacgagcc	240
natcctcggt	ganaagctgg	agagt				265

<210> 14

<211> 317

<212> DNA

<213> Homosapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> N=A,T,C or G

<400> 14

gatccggccn	cgcacganct	taccggtnaa	aacttcnncn	ccnataatat	ttgccgcgcg	60
agccgcctcg	angctctcgg	cgtaactccg	gatgcacggg	ggaccgtgac	ggttgtantg	120
ccctggcttt	tctcagenga	aatctgcaca	gccatcttcc	gatcgatctg	gcgcagggtg	180
ggcggcncaa	aacgggtggc	atctccaaac	cgcaggaacg	tgttttgcag	gatgtcgaac	240
atcatccacg	cttcggtncc	caacggctac	ttcgcccggg	accgggccat	gtcatcctcg	300
gtganaagct	ggnant					317

<210> 15

<211> 341

<212> DNA

<213> Homosapiens

<220>

<221> misc_feature

<222> (0)...(0)

<223> N=A,T,C or G

<400> 15

actctccagc	ctcgcaccga	ggatcagggc	gtcgtcgact	ccgtcgacct	gaccgcctcc	60
ccnccgctgc	tctcgatcgg	cggccagacc	tacaccancg	acgtagatca	agcgcgtggt	120
gcgcggcgcn	acnagcanca	nctaantcaa	ggcctcgctg	catcccgcga	atccagcgct	180
cagcttcgcg	ggaattgcgc	gancgctttt	gcgcgtcncg	agtnaccgca	tacacacctg	240

```

ccgtccctgc gaaagcaagg acccatactc cgngcgggt gttgttgacg ggactcgtca 300
tggcggcaac gcacaacgtn naacttctgt ggttatggat c 341

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<210> 16
<211> 256
<212> DNA
<213> Homosapiens

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<220>
<221> misc_feature
<222> (0)...(0)
<223> N=A,T,C or G

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<400> 16
gatccgcgca tcctctctgt ggctctcgcg gggtcagagg tggataaggc cggccgcaag 60
ctcggacttc ccgtcncaat cnaaggcttc tgcgacncc antacaacta cnacggcaat 120
ctnacatcac gcaagatcgc angctcngtc atcaaggacg cngcggtcnc cccccggcag 180
gtgctcnata tngtgttgaa naacaccatc gctcctgcaa cggcaagaag atcacatgca 240
aggtccactc gctgtg 256

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<210> 17
<211> 701
<212> DNA
<213> Homosapiens

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<220>
<223> N = A, T, C or G

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<400> 17
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ctaaacggag gatctcacga acatccgctc caaccccgac accacgctcc ccgccgtcac 120
gacaggctcg ctgccctcct cgcgcaagtt ctttgcaatc cctgaggccg cgcccgacat 180
ccgcgttccc ttgcgcgaga tcctcctgtc cgagggcgcc ggcgagccga acctgccggt 240
ctatgacacc tcggggccct acaccgatcc ggccgtgacg atcgacgtca acagcggcct 300
gccgcgcaat cgcctcgcct gggtcaggga acgcggcggc gtcgaggaat atcanggccg 360
caccatcaag ccggaggaca acggcaatgt cggcgcaccc caccgcgcca aggcgttcac 420
cgngcaccac aagccgctgc gcggnctcga cggcacaaga tcacccactc gagttcgccg 480
cgccggcatt ataccaagga gatgatctac gtcgccgagc gtgagaatct tggncgcaag 540
cagcagctng agcgcgcgga nggcccggctn gccgacggna agagttttg cgccgcgggtg 600
ccggncttna ttacgcgcga atttgtnccg aangagatcg ncgcggncgn gccattattt 660
cctttnaaaa ttaancattg ccgagcttga accgatgaan n 701

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<210> 18
<211> 511
<212> DNA
<213> Homosapiens

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<220>
<223> N=A,T,C or G

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<400> 18
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aaccggggac gagctggcct tcctgcccgc cgccctcgaa attgtcgaga cgccgccatc 120
tcccaccgcg agactcacgg ccgccttgct tgctgccttg ttctactgcg ccgtggcggtg 180
ggcgggtctc ggcaggatcg acatcgttgc ttctgcatcc agaaagatcg tgccggggcga 240
ccgtgtaaaag ctggttcagc cgctcgaggt cggcgtgggt cgggccactc atgtccgcga 300
tggccaaacc gtcaaggccg gcgagattct gatcgagctg gatccattcg cgggtgggtg 360
ggatgttgcg ccccgtcnag aggtccatca cgggtgctggc gcccancgg atcgccacac 420
catcttgctg acctnttctt caccgacgan gtcaccgccc agttgccgat attgcgntga 480
tcttantcan gaanntgcgg ncgatgatca t 511

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<210> 19
 <211> 620
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (1)...(618)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 19
 act ctc can cct ctc acc gag gat cag aat agg tga aga gcg aag aca 48
 Thr Leu Xaa Pro Leu Thr Glu Asp Gln Asn Arg * Arg Ala Lys Thr
 1 5 10 15
 ccg aga acg tct ggc ctt gaa cgg aca gcg tgc ttg agt tgg tcg ggg 96
 Pro Arg Thr Ser Gly Leu Glu Arg Thr Ala Cys Leu Ser Trp Ser Gly
 20 25 30
 tca cca ccg gac ccg tgt cca ccg gcg cag tca cng tga aag cac ttg 144
 Ser Pro Pro Asp Pro Cys Pro Pro Ala Gln Ser Xaa * Lys His Leu
 35 40 45
 acc atg atc cca gac ggt gcc gtc atc cgc gcg gac cca can cgt ntc 192
 Thr Met Ile Pro Asp Gly Ala Val Ile Arg Ala Asp Pro Xaa Arg Xaa
 50 55 60
 cgc gcc cga ccg gat tga tag ctc agc gac acc agc tgg gct gcc gtg 240
 Arg Ala Arg Pro Asp * * Leu Ser Asp Thr Ser Trp Ala Ala Val
 65 70 75
 acg tan ttg tgc tgg ttn ggt gca agt gcc acc ccg ctc aag aca aan 288
 Thr Xaa Leu Cys Trp Xaa Gly Ala Ser Ala Thr Pro Leu Lys Thr Xaa
 80 85 90
 tgg ccg cac ctg tgc ccg tgt ccc aaa cgt cat att ggg tcg cag cac 336
 Trp Pro His Leu Cys Pro Cys Pro Lys Arg His Ile Gly Ser Gln His
 95 100 105
 tgt cga acg gat cac tgt ang tgc aca gcg acn aan ccg cat anc tct 384
 Cys Arg Thr Asp His Cys Xaa Cys Thr Ala Thr Xaa Pro His Xaa Ser
 110 115 120
 ngc cgt ggg gcg caa cga tgt tnn aca ccg tct caa cgg gta ccg tgt 432
 Xaa Arg Gly Ala Gln Arg Cys Xaa Thr Pro Ser Gln Arg Val Pro Cys
 125 130 135 140
 cna ggg gan cat tta cng gga aag cat tcg acc act ccc cca cac cgt 480
 Xaa Gly Xaa His Leu Xaa Gly Lys His Ser Thr Thr Pro Pro His Arg
 145 150 155
 gcc cgc att tgc gcc gat tcc ttt cat tga tat gtc cac gtc ggt ngg 528
 Ala Arg Ile Cys Ala Asp Ser Phe His * Tyr Val His Val Gly Xaa
 160 165 170
 nct tta agc ngg cgg caa ccg cgg tgn agc tnc act ttt tgt tcc ttt 576
 Xaa Leu Ser Xaa Arg Gln Pro Arg Xaa Ser Xaa Thr Phe Cys Ser Phe
 175 180 185

tat tga ngg tta att tgc gcg ctt tgg ncg taa ntn ttt nga
 Tyr * Xaa Leu Ile Cys Ala Leu Trp Xaa * Xaa Phe Xaa
 190 195

618

an

620

<210> 20
 <211> 199
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 20
 Thr Leu Xaa Pro Leu Thr Glu Asp Gln Asn Arg Arg Ala Lys Thr Pro
 1 5 10 15
 Arg Thr Ser Gly Leu Glu Arg Thr Ala Cys Leu Ser Trp Ser Gly Ser
 20 25 30
 Pro Pro Asp Pro Cys Pro Pro Ala Gln Ser Xaa Lys His Leu Thr Met
 35 40 45
 Ile Pro Asp Gly Ala Val Ile Arg Ala Asp Pro Xaa Arg Xaa Arg Ala
 50 55 60
 Arg Pro Asp Leu Ser Asp Thr Ser Trp Ala Ala Val Thr Xaa Leu Cys
 65 70 75 80
 Trp Xaa Gly Ala Ser Ala Thr Pro Leu Lys Thr Xaa Trp Pro His Leu
 85 90 95
 Cys Pro Cys Pro Lys Arg His Ile Gly Ser Gln His Cys Arg Thr Asp
 100 105 110
 His Cys Xaa Cys Thr Ala Thr Xaa Pro His Xaa Ser Xaa Arg Gly Ala
 115 120 125
 Gln Arg Cys Xaa Thr Pro Ser Gln Arg Val Pro Cys Xaa Gly Xaa His
 130 135 140
 Leu Xaa Gly Lys His Ser Thr Thr Pro Pro His Arg Ala Arg Ile Cys
 145 150 155 160
 Ala Asp Ser Phe His Tyr Val His Val Gly Xaa Xaa Leu Ser Xaa Arg
 165 170 175
 Gln Pro Arg Xaa Ser Xaa Thr Phe Cys Ser Phe Tyr Xaa Leu Ile Cys
 180 185 190
 Ala Leu Trp Xaa Xaa Phe Xaa
 195

<210> 21
 <211> 620
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (2)...(619)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 21
 a ctc tcc anc ctc tca ccg agg atc aga ata ggt gaa gag cga aga cac
 Leu Ser Xaa Leu Ser Pro Arg Ile Arg Ile Gly Glu Glu Arg Arg His

49

1	5	10	15	
cga gaa cgt ctg gcc ttg aac gga cag cgt gct tga gtt ggt cgg ggt				97
Arg Glu Arg Leu Ala Leu Asn Gly Gln Arg Ala * Val Gly Arg Gly				
20		25	30	
cac cac cgg acc cgt gtc cac cgg cgc agt cac ngg gaa agc act tga				145
His His Arg Thr Arg Val His Arg Arg Ser His Xaa Glu Ser Thr *				
35		40	45	
cca tga tcc cag acg gtg ccg tca tcc gcg cgg acc cac anc gtn tcc				193
Pro * Ser Gln Thr Val Pro Ser Ser Ala Arg Thr His Xaa Val Ser				
50		55	60	
gcg ccc gac cgg att gat agc tca gcg aca cca gct ggg ctg ccg tga				241
Ala Pro Asp Arg Ile Asp Ser Ser Ala Thr Pro Ala Gly Leu Pro *				
65		70	75	
cgt ant tgt gct ggt tng gtg caa gtg cca ccc cgc tca aga caa ant				289
Arg Xaa Cys Ala Gly Xaa Val Gln Val Pro Pro Arg Ser Arg Gln Xaa				
80		85	90	
ggc cgc acc tgt gcc cgt gtc cca aac gtc ata ttg ggt cgc agc act				337
Gly Arg Thr Cys Ala Arg Val Pro Asn Val Ile Leu Gly Arg Ser Thr				
95		100	105	
gtc gaa cgg atc act gta ngg gca cag cga cna anc cgc ata nct ctn				385
Val Glu Arg Ile Thr Val Xaa Ala Gln Arg Xaa Xaa Arg Ile Xaa Leu				
110		115	120	
gcc gtg ggg cgc aac gat gtt nna cac cgt ctc aac ggg tac cgt gtc				433
Ala Val Gly Arg Asn Asp Val Xaa His Arg Leu Asn Gly Tyr Arg Val				
125		130	135	140
nag ggg anc att tac ngg gaa agc att cga cca ctc ccc cac acc gtg				481
Xaa Gly Xaa Ile Tyr Xaa Glu Ser Ile Arg Pro Leu Pro His Thr Val				
145		150	155	
ccc gca ttt gcg ccg att cct ttc att gat atg tcc acg tcg gtn ggn				529
Pro Ala Phe Ala Pro Ile Pro Phe Ile Asp Met Ser Thr Ser Val Gly				
160		165	170	
ctt taa gcn ggc ggc aac cgc ggt gna gct nca ctt ttt gtt cct ttt				577
Leu * Ala Gly Gly Asn Arg Gly Xaa Ala Xaa Leu Phe Val Pro Phe				
175		180	185	
att gan ggt taa ttt gcg cgc ttt ggn cgt aan tnt ttn gaa				619
Ile Xaa Gly * Phe Ala Arg Phe Gly Arg Xaa Xaa Xaa Glu				
190		195	200	
n				620

<210> 22

<211> 200

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 22

Leu Ser Xaa Leu Ser Pro Arg Ile Arg Ile Gly Glu Glu Arg Arg His
 1 5 10 15
 Arg Glu Arg Leu Ala Leu Asn Gly Gln Arg Ala Val Gly Arg Gly His
 20 25 30
 His Arg Thr Arg Val His Arg Arg Ser His Xaa Glu Ser Thr Pro Ser
 35 40 45
 Gln Thr Val Pro Ser Ser Ala Arg Thr His Xaa Val Ser Ala Pro Asp
 50 55 60
 Arg Ile Asp Ser Ser Ala Thr Pro Ala Gly Leu Pro Arg Xaa Cys Ala
 65 70 75 80
 Gly Xaa Val Gln Val Pro Pro Arg Ser Arg Gln Xaa Gly Arg Thr Cys
 85 90 95
 Ala Arg Val Pro Asn Val Ile Leu Gly Arg Ser Thr Val Glu Arg Ile
 100 105 110
 Thr Val Xaa Ala Gln Arg Xaa Xaa Arg Ile Xaa Leu Ala Val Gly Arg
 115 120 125
 Asn Asp Val Xaa His Arg Leu Asn Gly Tyr Arg Val Xaa Gly Xaa Ile
 130 135 140
 Tyr Xaa Glu Ser Ile Arg Pro Leu Pro His Thr Val Pro Ala Phe Ala
 145 150 155 160
 Pro Ile Pro Phe Ile Asp Met Ser Thr Ser Val Gly Leu Ala Gly Gly
 165 170 175
 Asn Arg Gly Xaa Ala Xaa Leu Phe Val Pro Phe Ile Xaa Gly Phe Ala
 180 185 190
 Arg Phe Gly Arg Xaa Xaa Xaa Glu
 195 200

<210> 23

<211> 620

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3)...(620)

<223> N= A, T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 23

ac tct cca ncc tct cac cga gga tca gaa tag gtg aag agc gaa gac 47
 Ser Pro Xaa Ser His Arg Gly Ser Glu * Val Lys Ser Glu Asp
 1 5 10
 acc gag aac gtc tgg cct tga acg gac agc gtg ctt gag ttg gtc ggg 95
 Thr Glu Asn Val Trp Pro * Thr Asp Ser Val Leu Glu Leu Val Gly
 15 20 25
 gtc acc acc gga ccc gtg tcc acc ggc gca gtc acn gtg aaa gca ctt 143
 Val Thr Thr Gly Pro Val Ser Thr Gly Ala Val Thr Val Lys Ala Leu
 30 35 40 45
 gac cat gat ccc aga cgg tgc cgt cat ccg cgc gga ccc aca ncg tnt 191
 Asp His Asp Pro Arg Arg Cys Arg His Pro Arg Gly Pro Thr Xaa Xaa
 50 55 60
 ccg cgc ccg acc gga ttg ata gct cag cga cac cag ctg ggc tgc cgt 239
 Pro Arg Pro Thr Gly Leu Ile Ala Gln Arg His Gln Leu Gly Cys Arg

65	70	75	
gac gta ntt gtg ctg gtt ngg tgc aag tgc cac ccc gct caa gac aaa			287
Asp Val Xaa Val Leu Val Xaa Cys Lys Cys His Pro Ala Gln Asp Lys			
80	85	90	
ntg gcc gca cct gtg ccc gtg tcc caa acg tca tat tgg gtc gca gca			335
Xaa Ala Ala Pro Val Pro Val Ser Gln Thr Ser Tyr Trp Val Ala Ala			
95	100	105	
ctg tcg aac gga tca ctg tan gtg cac agc gac naa ncc gca tan ctc			383
Leu Ser Asn Gly Ser Leu Xaa Val His Ser Asp Xaa Xaa Ala Xaa Leu			
110	115	120	
tng ccg tgg ggc gca acg atg ttn nac acc gtc tca acg ggt acc gtg			431
Xaa Pro Trp Gly Ala Thr Met Xaa Xaa Thr Val Ser Thr Gly Thr Val			
130	135	140	
tcn agg gga nca ttt acn ggg aaa gca ttc gac cac tcc ccc aca ccg			479
Ser Arg Gly Xaa Phe Thr Gly Lys Ala Phe Asp His Ser Pro Thr Pro			
145	150	155	
tgc ccg cat ttg cgc cga ttc ctt tca ttg ata tgt cca cgt cgg tng			527
Cys Pro His Leu Arg Arg Phe Leu Ser Leu Ile Cys Pro Arg Arg Xaa			
160	165	170	
gnc ttt aag cng gcg gca acc gcg gtg nag ctn cac ttt ttg ttc ctt			575
Xaa Phe Lys Xaa Ala Ala Thr Ala Val Xaa Leu His Phe Leu Phe Leu			
175	180	185	
tta ttg ang gtt aat ttg cgc gct ttg gnc gta ant ntt tng aan			620
Leu Leu Xaa Val Asn Leu Arg Ala Leu Xaa Val Xaa Xaa Xaa Xaa			
190	195	200	

<210> 24
 <211> 204
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence

<400> 24

Ser	Pro	Xaa	Ser	His	Arg	Gly	Ser	Glu	Val	Lys	Ser	Glu	Asp	Thr	Glu
1			5					10					15		
Asn	Val	Trp	Pro	Thr	Asp	Ser	Val	Leu	Glu	Leu	Val	Gly	Val	Thr	Thr
			20					25				30			
Gly	Pro	Val	Ser	Thr	Gly	Ala	Val	Thr	Val	Lys	Ala	Leu	Asp	His	Asp
			35				40					45			
Pro	Arg	Arg	Cys	Arg	His	Pro	Arg	Gly	Pro	Thr	Xaa	Xaa	Pro	Arg	Pro
			50			55					60				
Thr	Gly	Leu	Ile	Ala	Gln	Arg	His	Gln	Leu	Gly	Cys	Arg	Asp	Val	Xaa
65				70				75						80	
Val	Leu	Val	Xaa	Cys	Lys	Cys	His	Pro	Ala	Gln	Asp	Lys	Xaa	Ala	Ala
				85				90						95	
Pro	Val	Pro	Val	Ser	Gln	Thr	Ser	Tyr	Trp	Val	Ala	Ala	Leu	Ser	Asn
			100				105						110		
Gly	Ser	Leu	Xaa	Val	His	Ser	Asp	Xaa	Xaa	Ala	Xaa	Leu	Xaa	Pro	Trp

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<210> 25
<211> 619
<212> DNA
<213> Homosapiens
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 $\langle 220 \rangle$

<223> N= A, T, C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

[illegible]

```
<210> 26
<211> 200
<212> PRT
<213> Homosapiens
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<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 26																
Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Gln	Ser	Ala	Gln	Ile	Asn	Xaa	Gln	Lys	Glu	
1				5					10					15		
Gln	Lys	Val	Xaa	Xaa	His	Arg	Gly	Cys	Arg	Xaa	Leu	Lys	Xaa	Xaa	Pro	
			20					25					30			
Thr	Trp	Thr	Tyr	Gln	Lys	Glu	Ser	Ala	Gln	Met	Arg	Ala	Arg	Cys	Gly	
		35					40					45				
Gly	Val	Val	Glu	Cys	Phe	Pro	Xaa	Lys	Xaa	Ser	Pro	Xaa	His	Gly	Thr	
	50					55					60					
Arg	Asp	Gly	Xaa	Xaa	His	Arg	Cys	Ala	Pro	Arg	Xaa	Glu	Xaa	Cys	Xaa	
	65				70					75					80	
Xaa	Val	Ala	Val	His	Xaa	Gln	Ser	Val	Arg	Gln	Cys	Cys	Asp	Pro	Ile	

```

<210> 27
<211> 202
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 27
Phe Xaa Xaa Xaa Thr Xaa Lys Ala Arg Lys Leu Thr Xaa Asn Lys Arg
 1          5          10          15
Asn Lys Lys Xaa Ser Xaa Thr Ala Val Ala Ala Xaa Leu Lys Xaa Xaa
 20          25          30
Arg Arg Gly His Ile Asn Glu Arg Asn Arg Arg Lys Cys Gly His Gly
 35          40          45
Val Gly Glu Trp Ser Asn Ala Phe Xaa Val Asn Xaa Pro Xaa Asp Thr
 50          55          60
Val Pro Val Glu Thr Val Xaa Asn Ile Val Ala Pro His Gly Xaa Xaa
 65          70          75          80
Tyr Ala Xaa Xaa Ser Leu Cys Xaa Tyr Ser Asp Pro Phe Asp Ser Ala
 85          90          95
Ala Thr Gln Tyr Asp Val Trp Asp Thr Gly Thr Gly Ala Ala Xaa Leu
 100          105          110
Ser Ala Gly Trp His Leu His Xaa Thr Ser Thr Xaa Thr Ser Arg Gln
 115          120          125
Pro Ser Trp Cys Arg Ala Ile Asn Pro Val Gly Arg Gly Xaa Xaa Val
 130          135          140
Gly Pro Arg Gly Arg His Arg Leu Gly Ser Trp Ser Ser Ala Phe Xaa
 145          150          155          160
Val Thr Ala Pro Val Asp Thr Gly Pro Val Val Thr Pro Thr Asn Ser
 165          170          175
Ser Thr Leu Ser Val Gln Gly Gln Thr Phe Ser Val Ser Ser Leu Phe
 180          185          190
Thr Tyr Ser Asp Pro Arg Glu Xaa Gly Glu
 195          200

```

```
<210> 28
<211> 201
<212> PRT
<213> Homosapiens
```

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 28

```

Xaa Lys Xaa Leu Xaa Pro Lys Arg Ala Asn Xaa Ser Ile Lys Gly Thr
 1           5           10           15
Lys Ser Xaa Ala Xaa Pro Arg Leu Pro Xaa Ala Xaa Xaa Thr Asp Val
          20           25           30
Asp Ile Ser Met Lys Gly Ile Gly Ala Asn Ala Gly Thr Val Trp Gly
          35           40           45
Ser Gly Arg Met Leu Ser Xaa Met Xaa Pro Xaa Thr Arg Tyr Pro Leu
          50           55           60
Arg Arg Cys Xaa Thr Ser Leu Arg Pro Thr Xaa Arg Xaa Met Arg Xaa
65          70           75           80
Xaa Arg Cys Ala Xaa Thr Val Ile Arg Ser Thr Val Leu Arg Pro Asn
          85           90           95
Met Thr Phe Gly Thr Arg Ala Gln Val Arg Pro Xaa Cys Leu Glu Arg
          100          105          110
Gly Gly Thr Cys Thr Xaa Pro Ala Gln Xaa Arg His Gly Ser Pro Ala
          115          120          125
Gly Val Ala Glu Leu Ser Ile Arg Ser Gly Ala Xaa Thr Xaa Trp Val
          130          135          140
Arg Ala Asp Asp Gly Thr Val Trp Asp His Gly Gln Val Leu Ser Xaa
145          150          155          160
Leu Arg Arg Trp Thr Arg Val Arg Trp Pro Arg Pro Thr Gln Ala Arg
          165          170          175
Cys Pro Phe Lys Ala Arg Arg Ser Arg Cys Leu Arg Ser Ser Pro Ile
          180          185          190
Leu Ile Leu Gly Glu Arg Xaa Glu Ser
          195          200

```

<210> 29

<211> 662

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (1)...(660)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 29

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gat ccg acc agc aat cag gcg gag ctg cag cac ctg aaa aac gac ctt      48
Asp Pro Thr Ser Asn Gln Ala Glu Leu Gln His Leu Lys Asn Asp Leu
 1           5           10           15

ctc tcg gca ctg ctg ggt att tca cgc aac cgc tct gcg ctt ggc ggg      96
Leu Ser Ala Leu Leu Gly Ile Ser Arg Asn Arg Ser Ala Leu Gly Gly
          20           25           30

aaa cac cga cgc gct tga agg ctt acc gga cga cac gcc gcc agc ctt      144
Lys His Arg Arg Ala * Arg Leu Thr Gly Arg His Ala Ala Ser Leu
          35           40           45

```

gat tcg aat gca tct gga gta ctt gcg cag tca gga ttc cga gca gcg 192
 Asp Ser Asn Ala Ser Gly Val Leu Ala Gln Ser Gly Phe Arg Ala Ala
 50 55 60

cgc caa gct gtc cga act gga tca gca acg ggt gca gaa ggt cgc gga 240
 Arg Gln Ala Val Arg Thr Gly Ser Ala Thr Gly Ala Glu Gly Arg Gly
 65 70 75

gac cag gac gat cga cgc cag cat cgc gaa gat tga agc ttt gct gcg 288
 Asp Gln Asp Asp Arg Arg Gln His Arg Glu Asp * Ser Phe Ala Ala
 80 85 90

gtg ctg cag gan cgg gtc ggg gtt cgc aag tac ctg gcg gac agg gag 336
 Val Leu Gln Xaa Arg Val Gly Val Arg Lys Tyr Leu Ala Asp Arg Glu
 95 100 105 110

tac ggc tca aag ctg caa tat tcg cag gaa ctc cag gaa ctg gtc ggg 384
 Tyr Gly Ser Lys Leu Gln Tyr Ser Gln Glu Leu Gln Glu Leu Val Gly
 115 120 125

atg cag cag gac atc ctg gtg caa cgg agc aaa gct cga gga aac caa 432
 Met Gln Gln Asp Ile Leu Val Gln Arg Ser Lys Ala Arg Gly Asn Gln
 130 135 140

tgc ggn ttg tcg ccg cac ttc gac gaa aac ccg cgg naa gct tcg tct 480
 Cys Gly Leu Ser Pro His Phe Asp Glu Asn Pro Arg Xaa Ala Ser Ser
 145 150 155

nng aat aac cgg cac ccg nct gtt ccn acg atc ttg gcc caa ggg gac 528
 Xaa Asn Asn Arg His Pro Xaa Val Pro Thr Ile Leu Ala Gln Gly Asp
 160 165 170

gca aaa aag ggc cgg caa gnc ctc aaa gga cca agg gng ttt taa aan 576
 Ala Lys Lys Gly Arg Gln Xaa Leu Lys Gly Pro Arg Xaa Phe * Xaa
 175 180 185

ccg agc acc cgg gac cca acc ttt aaa aan cnt tgg cgg ccc cca ttc 624
 Pro Ser Thr Arg Asp Pro Thr Phe Lys Xaa Xaa Trp Arg Pro Pro Phe
 190 195 200 205

gac ggn gtg gng gca aca aat tgg gcc gng ccc cat tt 662
 Asp Gly Val Xaa Ala Thr Asn Trp Ala Xaa Pro His
 210 215

<210> 30
 <211> 217
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence

<400> 30
 Asp Pro Thr Ser Asn Gln Ala Glu Leu Gln His Leu Lys Asn Asp Leu
 1 5 10 15
 Leu Ser Ala Leu Leu Gly Ile Ser Arg Asn Arg Ser Ala Leu Gly Gly
 20 25 30
 Lys His Arg Arg Ala Arg Leu Thr Gly Arg His Ala Ala Ser Leu Asp

```

      35              40              45
Ser Asn Ala Ser Gly Val Leu Ala Gln Ser Gly Phe Arg Ala Ala Arg
  50              55              60
Gln Ala Val Arg Thr Gly Ser Ala Thr Gly Ala Glu Gly Arg Gly Asp
  65              70              75              80
Gln Asp Asp Arg Arg Gln His Arg Glu Asp Ser Phe Ala Ala Val Leu
      85              90              95
Gln Xaa Arg Val Gly Val Arg Lys Tyr Leu Ala Asp Arg Glu Tyr Gly
      100              105              110
Ser Lys Leu Gln Tyr Ser Gln Glu Leu Gln Glu Leu Val Gly Met Gln
      115              120              125
Gln Asp Ile Leu Val Gln Arg Ser Lys Ala Arg Gly Asn Gln Cys Gly
      130              135              140
Leu Ser Pro His Phe Asp Glu Asn Pro Arg Xaa Ala Ser Ser Xaa Asn
  145              150              155              160
Asn Arg His Pro Xaa Val Pro Thr Ile Leu Ala Gln Gly Asp Ala Lys
      165              170              175
Lys Gly Arg Gln Xaa Leu Lys Gly Pro Arg Xaa Phe Xaa Pro Ser Thr
      180              185              190
Arg Asp Pro Thr Phe Lys Xaa Xaa Trp Arg Pro Pro Phe Asp Gly Val
      195              200              205
Xaa Ala Thr Asn Trp Ala Xaa Pro His
      210              215

```

<210> 31

<211> 662

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (2)...(661)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 31

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g atc cga cca gca atc agg cgg agc tgc agc acc tga aaa acg acc ttc      49
  Ile Arg Pro Ala Ile Arg Arg Ser Cys Ser Thr * Lys Thr Thr Phe
    1              5              10              15

```

```

tct cgg cac tgc tgg gta ttt cac gca acc gct ctg cgc ttg gcg gga      97
Ser Arg His Cys Trp Val Phe His Ala Thr Ala Leu Arg Leu Ala Gly
      20              25              30

```

```

aac acc gac gcg ctt gaa ggc tta ccg gac gac acg ccg cca gcc ttg      145
Asn Thr Asp Ala Leu Glu Gly Leu Pro Asp Asp Thr Pro Pro Ala Leu
      35              40              45

```

```

att cga atg cat ctg gag tac ttg cgc agt cag gat tcc gag cag cgc      193
Ile Arg Met His Leu Glu Tyr Leu Arg Ser Gln Asp Ser Glu Gln Arg
      50              55              60

```

```

gcc aag ctg tcc gaa ctg gat cag caa cgg gtg cag aag gtc gcg gag      241
Ala Lys Leu Ser Glu Leu Asp Gln Gln Arg Val Gln Lys Val Ala Glu
      65              70              75

```

```

acc agg acg atc gac gcc agc atc gcg aag att gaa gct ttg ctg cgg      289
Thr Arg Thr Ile Asp Ala Ser Ile Ala Lys Ile Glu Ala Leu Leu Arg
      80              85              90              95

```


tgc tgc agg anc ggg tcg ggg ttc gca agt acc tgg cgg aca ggg agt 337
 Cys Cys Arg Xaa Gly Ser Gly Phe Ala Ser Thr Trp Arg Thr Gly Ser
 100 105 110
 acg gct caa agc tgc aat att cgc agg aac tcc agg aac tgg tcg gga 385
 Thr Ala Gln Ser Cys Asn Ile Arg Arg Asn Ser Arg Asn Trp Ser Gly
 115 120 125
 tgc agc agg aca tcc tgg tgc aac gga gca aag ctc gag gaa acc aat 433
 Cys Ser Arg Thr Ser Trp Cys Asn Gly Ala Lys Leu Glu Glu Thr Asn
 130 135 140
 gcg gnt tgt cgc cgc act tcg acg aaa acc cgc ggn aag ctt cgt ctn 481
 Ala Xaa Cys Arg Arg Thr Ser Thr Lys Thr Arg Gly Lys Leu Arg Leu
 145 150 155
 nga ata acc ggc acc cgn ctg ttc cna cga tct tgg ccc aag ggg acg 529
 Xaa Ile Thr Gly Thr Arg Leu Phe Xaa Arg Ser Trp Pro Lys Gly Thr
 160 165 170 175
 caa aaa agg gcc ggc aag ncc tca aag gac caa ggg ngc ttt aaa anc 577
 Gln Lys Arg Ala Gly Lys Xaa Ser Lys Asp Gln Gly Xaa Phe Lys Xaa
 180 185 190
 cga gca ccc ggg acc caa cct tta aaa anc ntt ggc ggc ccc cat tcg 625
 Arg Ala Pro Gly Thr Gln Pro Leu Lys Xaa Xaa Gly Gly Pro His Ser
 195 200 205
 acg gng tgg ngg caa caa att ggg ccg ngc ccc att t 662
 Thr Xaa Trp Xaa Gln Gln Ile Gly Pro Xaa Pro Ile
 210 215

<210> 32
 <211> 219
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 32
 Ile Arg Pro Ala Ile Arg Arg Ser Cys Ser Thr Lys Thr Thr Phe Ser
 1 5 10 15
 Arg His Cys Trp Val Phe His Ala Thr Ala Leu Arg Leu Ala Gly Asn
 20 25 30
 Thr Asp Ala Leu Glu Gly Leu Pro Asp Asp Thr Pro Pro Ala Leu Ile
 35 40 45
 Arg Met His Leu Glu Tyr Leu Arg Ser Gln Asp Ser Glu Gln Arg Ala
 50 55 60
 Lys Leu Ser Glu Leu Asp Gln Gln Arg Val Gln Lys Val Ala Glu Thr
 65 70 75 80
 Arg Thr Ile Asp Ala Ser Ile Ala Lys Ile Glu Ala Leu Leu Arg Cys
 85 90 95
 Cys Arg Xaa Gly Ser Gly Phe Ala Ser Thr Trp Arg Thr Gly Ser Thr
 100 105 110
 Ala Gln Ser Cys Asn Ile Arg Arg Asn Ser Arg Asn Trp Ser Gly Cys
 115 120 125

Ser Arg Thr Ser Trp Cys Asn Gly Ala Lys Leu Glu Glu Thr Asn Ala
 130 135 140
 Xaa Cys Arg Arg Thr Ser Thr Lys Thr Arg Gly Lys Leu Arg Leu Xaa
 145 150 155 160
 Ile Thr Gly Thr Arg Leu Phe Xaa Arg Ser Trp Pro Lys Gly Thr Gln
 165 170 175
 Lys Arg Ala Gly Lys Xaa Ser Lys Asp Gln Gly Xaa Phe Lys Xaa Arg
 180 185 190
 Ala Pro Gly Thr Gln Pro Leu Lys Xaa Xaa Gly Gly Pro His Ser Thr
 195 200 205
 Xaa Trp Xaa Gln Gln Ile Gly Pro Xaa Pro Ile
 210 215

<210> 33
 <211> 662
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (3)...(662)
 <223> N= A,T,C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 33
 ga tcc gac cag caa tca ggc gga gct gca gca cct gaa aaa cga cct 47
 Ser Asp Gln Gln Ser Gly Gly Ala Ala Ala Pro Glu Lys Arg Pro
 1 5 10 15
 tct ctc ggc act gct ggg tat ttc acg caa ccg ctc tgc gct tgg cgg 95
 Ser Leu Gly Thr Ala Gly Tyr Phe Thr Gln Pro Leu Cys Ala Trp Arg
 20 25 30
 gaa aca ccg acg cgc ttg aag gct tac cgg acg aca cgc cgc cag cct 143
 Glu Thr Pro Thr Arg Leu Lys Ala Tyr Arg Thr Thr Arg Arg Gln Pro
 35 40 45
 tga ttc gaa tgc atc tgg agt act tgc gca gtc agg att ccg agc agc 191
 * Phe Glu Cys Ile Trp Ser Thr Cys Ala Val Arg Ile Pro Ser Ser
 50 55 60
 gcg cca agc tgt ccg aac tgg atc agc aac ggg tgc aga agg tcg cgg 239
 Ala Pro Ser Cys Pro Asn Trp Ile Ser Asn Gly Cys Arg Arg Ser Arg
 65 70 75
 aga cca gga cga tcg acg cca gca tcg cga aga ttg aag ctt tgc tgc 287
 Arg Pro Gly Arg Ser Thr Pro Ala Ser Arg Arg Leu Lys Leu Cys Cys
 80 85 90
 ggt gct gca gga ncg ggt cgg ggt tcg caa gta cct ggc gga cag gga 335
 Gly Ala Ala Gly Xaa Gly Arg Gly Ser Gln Val Pro Gly Gly Gln Gly
 95 100 105 110
 gta cgg ctc aaa gct gca ata ttc gca gga act cca gga act ggt cgg 383
 Val Arg Leu Lys Ala Ala Ile Phe Ala Gly Thr Pro Gly Thr Gly Arg
 115 120 125
 gat gca gca gga cat cct ggt gca acg gag caa agc tcg agg aaa cca 431
 Asp Ala Ala Gly His Pro Gly Ala Thr Glu Gln Ser Ser Arg Lys Pro

130 135 140

atg cgg ntt gtc gcc gca ctt cga cga aaa ccc gcg gna agc ttc gtc 479
 Met Arg Xaa Val Ala Ala Leu Arg Arg Lys Pro Ala Xaa Ser Phe Val
 145 150 155

tnn gaa taa ccg gca ccc gnc tgt tcc nac gat ctt ggc cca agg gga 527
 Xaa Glu * Pro Ala Pro Xaa Cys Ser Xaa Asp Leu Gly Pro Arg Gly
 160 165 170

cgc aaa aaa ggg ccg gca agn cct caa agg acc aag ggn gtt tta aaa 575
 Arg Lys Lys Gly Pro Ala Xaa Pro Gln Arg Thr Lys Gly Val Leu Lys
 175 180 185

ncc gag cac ccg gga ccc aac ctt taa aaa ncn ttg gcg gcc ccc att 623
 Xaa Glu His Pro Gly Pro Asn Leu * Lys Xaa Leu Ala Ala Pro Ile
 190 195 200

cga cgg ngg ggn ggc aac aaa ttg ggc cgn gcc cca ttt 662
 Arg Arg Xaa Gly Gly Asn Lys Leu Gly Arg Ala Pro Phe
 205 210 215

<210> 34
 <211> 217
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 34

Ser Asp Gln Gln Ser Gly Gly Ala Ala Ala Pro Glu Lys Arg Pro Ser
 1 5 10 15
 Leu Gly Thr Ala Gly Tyr Phe Thr Gln Pro Leu Cys Ala Trp Arg Glu
 20 25 30
 Thr Pro Thr Arg Leu Lys Ala Tyr Arg Thr Thr Arg Arg Gln Pro Phe
 35 40 45
 Glu Cys Ile Trp Ser Thr Cys Ala Val Arg Ile Pro Ser Ser Ala Pro
 50 55 60
 Ser Cys Pro Asn Trp Ile Ser Asn Gly Cys Arg Arg Ser Arg Arg Pro
 65 70 75 80
 Gly Arg Ser Thr Pro Ala Ser Arg Arg Leu Lys Leu Cys Cys Gly Ala
 85 90 95
 Ala Gly Xaa Gly Arg Gly Ser Gln Val Pro Gly Gly Gln Gly Val Arg
 100 105 110
 Leu Lys Ala Ala Ile Phe Ala Gly Thr Pro Gly Thr Gly Arg Asp Ala
 115 120 125
 Ala Gly His Pro Gly Ala Thr Glu Gln Ser Ser Arg Lys Pro Met Arg
 130 135 140
 Xaa Val Ala Ala Leu Arg Lys Pro Ala Xaa Ser Phe Val Xaa Glu
 145 150 155 160
 Pro Ala Pro Xaa Cys Ser Xaa Asp Leu Gly Pro Arg Gly Arg Lys Lys
 165 170 175
 Gly Pro Ala Xaa Pro Gln Arg Thr Lys Gly Val Leu Lys Xaa Glu His
 180 185 190
 Pro Gly Pro Asn Leu Lys Xaa Leu Ala Ala Pro Ile Arg Arg Xaa Gly
 195 200 205
 Gly Asn Lys Leu Gly Arg Ala Pro Phe

210

215

<210> 35
 <211> 661
 <212> DNA
 <213> Homosapiens

<220>
 <223> N= A, T, C or G

<223> Frame shift sequence

<223> Reverse strand

<400> 35
 aaatggggcn cggcccaatt tgttgccncc acnccgtcga atggggggccg ccaangnttt 60
 ttaaagggtt ggtcccgggt gctcggnttt taaaacnccc ttggtccttt gaggncttgc 120
 cggccctttt ttgcgtcccc ttgggccaag atcgtnggaa cagncgggtg ccggttattc 180
 nnagacgaag cttncgcggg gttttcgtcg aagtgcggcg acaanccgca ttgggttccct 240
 cgagctttgc tccgttgac caggatgtcc tgctgcatcc cgaccagttc ctggagttcc 300
 tgcgaatatt gcagctttga gccgtactcc ctgtccgccg ggtacttgcg aaccgcagcc 360
 gntcctgcag caccgcagca aagcttcaat cttcgcgatg ctggcgtcga tcgtcctggt 420
 ctccgcgacc ttctgcaccc gttgctgac cagttcggac agcttggcgc gctgctcgga 480
 atcctgactg cgcaagtact ccagatgcat tcgaatcaag gctggcggcg tgctgctccgg 540
 taagccttca agcgcgtcgg tgtttccgcg caagcgcaga gcggttgctg gaaataccca 600
 gcagtgccga gagaaggctg tttttcaggt gctgcagctc cgctgattg ctggtcggat 660
 c 661

<210> 36
 <211> 218
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 36
 Lys Trp Gly Xaa Ala Gln Phe Val Ala Xaa Xaa Pro Ser Asn Gly Gly
 1 5 10 15
 Arg Gln Xaa Phe Leu Lys Val Gly Ser Arg Val Leu Xaa Phe Asn Xaa
 20 25 30
 Leu Gly Pro Leu Arg Xaa Cys Arg Pro Phe Phe Ala Ser Pro Trp Ala
 35 40 45
 Lys Ile Xaa Gly Thr Xaa Gly Cys Arg Leu Phe Xaa Asp Glu Ala Xaa
 50 55 60
 Arg Gly Phe Ser Ser Lys Cys Gly Asp Xaa Pro His Trp Phe Pro Arg
 65 70 75 80
 Ala Leu Leu Arg Cys Thr Arg Met Ser Cys Cys Ile Pro Thr Ser Ser
 85 90 95
 Trp Ser Ser Cys Glu Tyr Cys Ser Phe Glu Pro Tyr Ser Leu Ser Ala
 100 105 110
 Arg Tyr Leu Arg Thr Pro Thr Xaa Ser Cys Ser Thr Ala Ala Lys Leu
 115 120 125
 Gln Ser Ser Arg Cys Trp Arg Ser Ser Trp Ser Pro Arg Pro Ser
 130 135 140
 Ala Pro Val Ala Asp Pro Val Arg Thr Ala Trp Arg Ala Ala Arg Asn
 145 150 155 160

Pro Asp Cys Ala Ser Thr Pro Asp Ala Phe Glu Ser Arg Leu Ala Ala
 165 170 175
 Cys Arg Pro Val Ser Leu Gln Ala Arg Arg Cys Phe Pro Pro Ser Ala
 180 185 190
 Glu Arg Leu Arg Glu Ile Pro Ser Ala Glu Arg Arg Ser Phe Phe
 195 200 205
 Arg Cys Cys Ser Ser Ala Leu Leu Val Gly
 210 215

<210> 37
 <211> 217
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 37
 Asn Gly Xaa Arg Pro Asn Leu Leu Xaa Pro Xaa Arg Arg Met Gly Ala
 1 5 10 15
 Ala Xaa Xaa Phe Arg Leu Gly Pro Gly Cys Ser Xaa Phe Lys Xaa Pro
 20 25 30
 Leu Val Leu Xaa Leu Ala Gly Pro Phe Leu Arg Pro Leu Gly Pro Arg
 35 40 45
 Ser Xaa Glu Gln Xaa Gly Ala Gly Tyr Xaa Xaa Thr Lys Leu Xaa Ala
 50 55 60
 Gly Phe Arg Arg Ser Ala Ala Thr Xaa Arg Ile Gly Phe Leu Glu Leu
 65 70 75 80
 Cys Ser Val Ala Pro Gly Cys Pro Ala Ala Ser Arg Pro Val Pro Gly
 85 90 95
 Val Pro Ala Asn Ile Ala Ala Leu Ser Arg Thr Pro Cys Pro Pro Gly
 100 105 110
 Thr Cys Glu Pro Arg Pro Xaa Pro Ala Ala Pro Gln Gln Ser Phe Asn
 115 120 125
 Leu Arg Asp Ala Gly Val Asp Arg Pro Gly Leu Arg Asp Leu Leu His
 130 135 140
 Pro Leu Leu Ile Gln Phe Gly Gln Leu Gly Ala Leu Leu Gly Ile Leu
 145 150 155 160
 Thr Ala Gln Val Leu Gln Met His Ser Asn Gln Gly Trp Arg Arg Val
 165 170 175
 Val Arg Ala Phe Lys Arg Val Gly Val Ser Arg Gln Ala Gln Ser Gly
 180 185 190
 Cys Val Lys Tyr Pro Ala Asx Pro Arg Trp Gly Arg Phe Ser Gly Ala
 195 200 205
 Ala Ala Pro Pro Asp Cys Trp Ser Asp
 210 215

<210> 38
 <211> 217
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 38

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Met Gly Xaa Gly Pro Ile Cys Cys Xaa His Xaa Val Glu Trp Gly Pro
1          5          10          15
Pro Xaa Xaa Phe Lys Gly Trp Val Pro Gly Ala Arg Xaa Leu Lys Xaa
20          25          30
Pro Trp Ser Phe Glu Xaa Leu Pro Ala Leu Phe Cys Val Pro Leu Gly
35          40          45
Gln Asp Arg Xaa Asn Xaa Arg Val Pro Val Val Ile Xaa Arg Arg Ser
50          55          60
Xaa Pro Arg Val Phe Val Glu Val Arg Arg Gln Xaa Ala Leu Val Ser
65          70          75          80
Ser Ser Phe Ala Pro Leu His Gln Asp Val Leu Leu His Pro Asp Gln
85          90          95
Phe Leu Glu Phe Leu Arg Ile Leu Gln Leu Ala Val Leu Pro Val Arg
100         105         110
Gln Val Leu Ala Asn Pro Asp Pro Xaa Leu Gln His Arg Ser Lys Ala
115         120         125
Ser Ile Phe Ala Met Leu Ala Ser Ile Val Leu Val Ser Ala Thr Phe
130         135         140
Cys Thr Arg Cys Ser Ser Ser Asp Ser Leu Ala Arg Cys Ser Glu Ser
145         150         155         160
Leu Arg Lys Tyr Ser Arg Cys Ile Arg Ile Lys Ala Gly Gly Val Ser
165         170         175
Ser Gly Lys Pro Ser Ser Ala Ser Val Phe Pro Ala Lys Arg Arg Ala
180         185         190
Val Ala Asn Thr Gln Gln Cys Arg Glu Lys Val Val Phe Gln Val Leu
195         200         205
Gln Leu Arg Leu Ile Ala Gly Arg Ile
210         215

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<210> 39

<211> 191

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (1)...(189)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 39

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cgc gct gga cta tcn cta aag ggt ctc cna cna cgt cca ncc gga cna      48
Arg Ala Gly Leu Ser Leu Lys Gly Leu Xaa Xaa Arg Pro Xaa Gly Xaa
1          5          10          15

gct gac ctc gtt tcc ncn aag cgt gaa act gaa ggc cgg tga aac cnt      96
Ala Asp Leu Val Ser Xaa Lys Arg Glu Thr Glu Gly Arg * Asn Xaa
20          25          30

cnt gtt cgc ctn gat cac cta cta gtc gcg cgc cnn gcg cga cag gat      144
Xaa Val Arg Leu Asp His Leu Leu Val Ala Arg Xaa Ala Arg Gln Asp
35          40          45

caa cgc caa ggt gat ggc cga tcc ccg cct ggc gtc gtc gat gga      189
Gln Arg Gln Gly Asp Gly Arg Ser Pro Pro Gly Val Val Asp Gly
50          55          60

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tc

<210> 40
 <211> 62
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 40
 Arg Ala Gly Leu Ser Leu Lys Gly Leu Xaa Xaa Arg Pro Xaa Gly Xaa
 1 5 10 15
 Ala Asp Leu Val Ser Xaa Lys Arg Glu Thr Glu Gly Arg Asn Xaa Xaa
 20 25 30
 Val Arg Leu Asp His Leu Leu Val Ala Arg Xaa Ala Arg Gln Asp Gln
 35 40 45
 Arg Gln Gly Asp Gly Arg Ser Pro Pro Gly Val Val Asp Gly
 50 55 60

<210> 41
 <211> 191
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (2)...(191)
 <223> N= A,T,C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 41
 c gcg ctg gac tat cnc taa agg gtc tcc nac nac gtc can ccg gac nag 49
 Ala Leu Asp Tyr Xaa * Arg Val Ser Xaa Xaa Val Xaa Pro Asp Xaa
 1 5 10 15
 ctg acc tcg ttt ccn cna agc gtg aaa ctg aag gcc ggt gaa acc ntc 97
 Leu Thr Ser Phe Pro Xaa Ser Val Lys Leu Lys Ala Gly Glu Thr Xaa
 20 25 30
 ntg ttc gcc tng atc acc tac tag tcg cgc gcc nng cgc gac agg atc 145
 Xaa Phe Ala Xaa Ile Thr Tyr * Ser Arg Ala Xaa Arg Asp Arg Ile
 35 40 45
 aac gcc aag gtg atg gcc gat ccc cgc ctg gcg tcg tcg atg gat c 191
 Asn Ala Lys Val Met Ala Asp Pro Arg Leu Ala Ser Ser Met Asp
 50 55 60

<210> 42
 <211> 61
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 42

Ala	Leu	Asp	Tyr	Xaa	Arg	Val	Ser	Xaa	Xaa	Val	Xaa	Pro	Asp	Xaa	Leu
1				5				10						15	
Thr	Ser	Phe	Pro	Xaa	Ser	Val	Lys	Leu	Lys	Ala	Gly	Glu	Thr	Xaa	Xaa
			20				25						30		
Phe	Ala	Xaa	Ile	Thr	Tyr	Ser	Arg	Ala	Xaa	Arg	Asp	Arg	Ile	Asn	Ala
		35				40					45				
Lys	Val	Met	Ala	Asp	Pro	Arg	Leu	Ala	Ser	Ser	Met	Asp			
	50				55						60				

<210> 43

<211> 191

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3)...(191)

<223> N= A,T,C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 43

cg	cgc	tgg	act	atc	nct	aaa	ggg	tct	ccn	acn	acg	tcc	anc	cgg	acn	47
	Arg	Trp	Thr	Ile	Xaa	Lys	Gly	Ser	Pro	Thr	Thr	Ser	Xaa	Arg	Thr	
1					5				10					15		
agc	tga	cct	cgt	ttc	cnc	naa	gcg	tga	aac	tga	agg	ccg	gtg	aaa	ccn	95
Ser	*	Pro	Arg	Phe	Xaa	Xaa	Ala	*	Asn	*	Arg	Pro	Val	Lys	Pro	
					20						25					
tcn	tgt	tcg	cct	nga	tca	cct	act	agt	cgc	gcg	ccn	ngc	gcg	aca	gga	143
Ser	Cys	Ser	Pro	Xaa	Ser	Pro	Thr	Ser	Arg	Ala	Pro	Xaa	Ala	Thr	Gly	
	30				35				40							
tca	acg	cca	agg	tga	tgg	ccg	atc	ccc	gcc	tgg	cgt	cgt	cga	tgg	atc	191
Ser	Thr	Pro	Arg	*	Trp	Pro	Ile	Pro	Ala	Trp	Arg	Arg	Arg	Trp	Ile	
	45				50				55							

<210> 44

<211> 59

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 44

Arg	Trp	Thr	Ile	Xaa	Lys	Gly	Ser	Pro	Thr	Thr	Ser	Xaa	Arg	Thr	Ser
1				5				10						15	
Pro	Arg	Phe	Xaa	Xaa	Ala	Asn	Arg	Pro	Val	Lys	Pro	Ser	Cys	Ser	Pro
			20				25					30			
Xaa	Ser	Pro	Thr	Ser	Arg	Ala	Pro	Xaa	Ala	Thr	Gly	Ser	Thr	Pro	Arg
	35				40						45				

Trp Pro Ile Pro Ala Trp Arg Arg Arg Trp Ile
50 55

<210> 45
<211> 190
<212> DNA
<213> Homosapiens

<220>
<223> N= A,T,C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 45
gatccatcga cgacgccagg cgggatcggc catcaccttg gcgttgatcc tgtcgcgcnn 60
ggcgcgcgac tagtaggtga tcnaggcgaa canganggtt tcaccggcct tcagtttcac 120
gcttngnga aacgaggtca gctngtccgg ntggacgtng tnggagaccc tttagnata 180
gtccagcgcg 190

<210> 46
<211> 61
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 46
Asp Pro Ser Thr Thr Pro Gly Gly Asp Arg Pro Ser Pro Trp Arg Ser
1 5 10 15
Cys Arg Xaa Xaa Arg Ala Thr Ser Arg Xaa Arg Arg Thr Xaa Xaa Phe
20 25 30
His Arg Pro Ser Val Ser Arg Xaa Xaa Glu Thr Arg Ser Ala Xaa Pro
35 40 45
Xaa Gly Arg Xaa Xaa Arg Pro Phe Xaa Asp Ser Pro Ala
50 55 60

<210> 47
<211> 63
<212> PRT
<213> Homosapiens

<220>
<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 47
Ile His Arg Arg Arg Gln Ala Gly Ile Gly His His Leu Gly Val Asp
1 5 10 15
Pro Val Ala Xaa Gly Ala Arg Leu Val Gly Asp Xaa Gly Glu Xaa Xaa
20 25 30
Gly Phe Thr Gly Leu Gln Phe His Ala Xaa Xaa Lys Arg Gly Gln Xaa

35 40 45
 Val Arg Xaa Asp Xaa Xaa Gly Asp Pro Leu Xaa Ile Val Gln Arg
 50 55 60

<210> 48
 <211> 59
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 48
 Ser Ile Asp Asp Ala Arg Arg Gly Ser Ala Ile Thr Leu Ala Leu Ile
 1 5 10 15
 Leu Ser Arg Xaa Ala Arg Asp Val Ile Xaa Ala Asn Xaa Xaa Val Ser
 20 25 30
 Pro Ala Phe Ser Phe Thr Leu Xaa Gly Asn Glu Val Ser Xaa Ser Xaa
 35 40 45
 Trp Thr Xaa Xaa Glu Thr Leu Xaa Ser Ser Ala
 50 55

<210> 49
 <211> 552
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (1)...(552)
 <223> N= A,T,C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 49
 gat ccg ctc gat gcc cag gcc cag tac agc gaa ctg ttc gcc cat ggc 48
 Asp Pro Leu Asp Ala Gln Ala Gln Tyr Ser Glu Leu Phe Ala His Gly
 1 5 10 15
 cgc gcc acg tca ctg ttg cta ttc gaa cat gtt cac ggt gaa tcc cgt 96
 Arg Ala Thr Ser Leu Leu Leu Phe Glu His Val His Gly Glu Ser Arg
 20 25 30
 gac cgc ggc cag gcg atg gtg gac ctg ctg gcg cag tac gag cag cac 144
 Asp Arg Gly Gln Ala Met Val Asp Leu Leu Ala Gln Tyr Glu Gln His
 35 40 45
 ggt ttg cag tta aac agc cgc gaa tta ccg gac cac ctg ccg ctg tat 192
 Gly Leu Gln Leu Asn Ser Arg Glu Leu Pro Asp His Leu Pro Leu Tyr
 50 55 60
 ctg gag tac ctg tcg cag ctg ccg caa ggc gaa gcc gtg gaa ggt ttg 240
 Leu Glu Tyr Leu Ser Gln Leu Pro Gln Gly Glu Ala Val Glu Gly Leu
 65 70 75 80
 aaa gat atc gcg ccg att ctg gca ttg ctg agc gcg cgt ctg caa cag 288

Lys	Asp	Ile	Ala	Pro	Ile	Leu	Ala	Leu	Leu	Ser	Ala	Arg	Leu	Gln	Gln		
				85					90					95			
cgt	gaa	agc	cgt	tat	gcc	gtg	atg	ttt	gat	ctg	ctg	ctg	aaa	ttg	gcc		336
Arg	Glu	Ser	Arg	Tyr	Ala	Val	Met	Phe	Asp	Leu	Leu	Leu	Lys	Leu	Ala		
			100					105					110				
gat	acc	gct	atc	gac	agc	gac	aaa	gtg	gcg	gaa	aaa	att	gcc	gac	gaa		384
Asp	Thr	Ala	Ile	Asp	Ser	Asp	Lys	Val	Ala	Glu	Lys	Ile	Ala	Asp	Glu		
		115					120					125					
gcg	cg	gat	gat	acg	ccg	cag	gcg	ctg	gat	gct	gtt	tgg	gaa	gaa	gag		432
Ala	Arg	Asp	Asp	Thr	Pro	Gln	Ala	Leu	Asp	Ala	Val	Trp	Glu	Glu	Glu		
	130					135					140						
cag	gtt	aaa	ttc	ttt	gct	gac	aaa	ggc	tgc	ggc	gat	tca	gca	atc	act		480
Gln	Val	Lys	Phe	Phe	Ala	Asp	Lys	Gly	Cys	Gly	Asp	Ser	Ala	Ile	Thr		
145					150				155					160			
gct	cat	cag	cgt	cgc	ttt	gcc	ggt	gcc	gtc	gcg	ccg	caa	tat	ctg	aat		528
Ala	His	Gln	Arg	Arg	Phe	Ala	Gly	Ala	Val	Ala	Pro	Gln	Tyr	Leu	Asn		
			165					170						175			
atc	ctc	ggt	gag	agg	ctg	gag	agt										552
Ile	Leu	Gly	Glu	Arg	Leu	Glu	Ser										
			180														

<210> 50
 <211> 184
 <212> PRT
 <213> Homosapiens

<220>
 <223> Frame shift sequence

<223> Frame shift sequence

<400>	50																
Asp	Pro	Leu	Asp	Ala	Gln	Ala	Gln	Tyr	Ser	Glu	Leu	Phe	Ala	His	Gly		
1				5					10					15			
Arg	Ala	Thr	Ser	Leu	Leu	Leu	Phe	Glu	His	Val	His	Gly	Glu	Ser	Arg		
			20					25					30				
Asp	Arg	Gly	Gln	Ala	Met	Val	Asp	Leu	Leu	Ala	Gln	Tyr	Glu	Gln	His		
		35					40					45					
Gly	Leu	Gln	Leu	Asn	Ser	Arg	Glu	Leu	Pro	Asp	His	Leu	Pro	Leu	Tyr		
	50					55					60						
Leu	Glu	Tyr	Leu	Ser	Gln	Leu	Pro	Gln	Gly	Glu	Ala	Val	Glu	Gly	Leu		
65					70					75				80			
Lys	Asp	Ile	Ala	Pro	Ile	Leu	Ala	Leu	Leu	Ser	Ala	Arg	Leu	Gln	Gln		
				85					90					95			
Arg	Glu	Ser	Arg	Tyr	Ala	Val	Met	Phe	Asp	Leu	Leu	Leu	Lys	Leu	Ala		
			100					105					110				
Asp	Thr	Ala	Ile	Asp	Ser	Asp	Lys	Val	Ala	Glu	Lys	Ile	Ala	Asp	Glu		
		115					120					125					
Ala	Arg	Asp	Asp	Thr	Pro	Gln	Ala	Leu	Asp	Ala	Val	Trp	Glu	Glu	Glu		
	130					135					140						
Gln	Val	Lys	Phe	Phe	Ala	Asp	Lys	Gly	Cys	Gly	Asp	Ser	Ala	Ile	Thr		
145					150				155					160			
Ala	His	Gln	Arg	Arg	Phe	Ala	Gly	Ala	Val	Ala	Pro	Gln	Tyr	Leu	Asn		
			165					170						175			

Ile Leu Gly Glu Arg Leu Glu Ser
180

<210> 51
<211> 552
<212> DNA
<213> Homosapiens

<220>
<221> CDS
<222> (2)...(552)
<223> N= A,T, C or G
Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 51
g atc cgc tcg atg ccc agg ccc agt aca gcg aac tgt tcg ccc atg gcc 49
Ile Arg Ser Met Pro Arg Pro Ser Thr Ala Asn Cys Ser Pro Met Ala
1 5 10 15

gcg cca cgt cac tgt tgc tat tcg aac atg ttc acg gtg aat ccc gtg 97
Ala Pro Arg His Cys Cys Tyr Ser Asn Met Phe Thr Val Asn Pro Val
20 25 30

acc gcg gcc agg cga tgg tgg acc tgc tgg cgc agt acg agc agc acg 145
Thr Ala Ala Arg Arg Trp Trp Thr Cys Trp Arg Ser Thr Ser Ser Thr
35 40 45

gtt tgc agt taa aca gcc gcg aat tac cgg acc acc tgc cgc tgt atc 193
Val Cys Ser * Thr Ala Ala Asn Tyr Arg Thr Thr Cys Arg Cys Ile
50 55 60

tgg agt acc tgt cgc agc tgc cgc aag gcg aag ccg tgg aag gtt tga 241
Trp Ser Thr Cys Arg Ser Cys Arg Lys Ala Lys Pro Trp Lys Val *
65 70 75

aag ata tcg cgc cga ttc tgg cat tgc tga gcg cgc gtc tgc aac agc 289
Lys Ile Ser Arg Arg Phe Trp His Cys * Ala Arg Val Cys Asn Ser
80 85 90

gtg aaa gcc gtt atg ccg tga tgt ttg atc tgc tgc tga aat tgg ccg 337
Val Lys Ala Val Met Pro * Cys Leu Ile Cys Cys * Asn Trp Pro
95 100 105

ata ccg cta tcg aca gcg aca aag tgg cgg aaa aaa ttg ccg acg aag 385
Ile Pro Leu Ser Thr Ala Thr Lys Trp Arg Lys Lys Leu Pro Thr Lys
110 115 120

cgc gcg atg ata cgc cgc agg cgc tgg atg ctg ttt ggg aag aag agc 433
Arg Ala Met Ile Arg Arg Arg Arg Trp Met Leu Phe Gly Lys Lys Ser
125 130 135

agg tta aat tct ttg ctg aca aag gct gcg gcg att cag caa tca ctg 481
Arg Leu Asn Ser Leu Leu Thr Lys Ala Ala Ala Ile Gln Gln Ser Leu
140 145 150 155

ctc atc agc gtc gct ttg ccg gtg ccg tcg cgc cgc aat atc tga ata 529
Leu Ile Ser Val Ala Leu Pro Val Pro Ser Arg Arg Asn Ile * Ile
160 165 170

tcc tcg gtg aga ggc tgg aga gt
 Ser Ser Val Arg Gly Trp Arg
 175

552

<210> 52
 <211> 177
 <212> PRT
 <213> Homosapiens

<220>
 <223> Frame shift sequence

<400> 52
 Ile Arg Ser Met Pro Arg Pro Ser Thr Ala Asn Cys Ser Pro Met Ala
 1 5 10 15
 Ala Pro Arg His Cys Cys Tyr Ser Asn Met Phe Thr Val Asn Pro Val
 20 25 30
 Thr Ala Ala Arg Arg Trp Trp Thr Cys Trp Arg Ser Thr Ser Ser Thr
 35 40 45
 Val Cys Ser Thr Ala Ala Asn Tyr Arg Thr Thr Cys Arg Cys Ile Trp
 50 55 60
 Ser Thr Cys Arg Ser Cys Arg Lys Ala Lys Pro Trp Lys Val Lys Ile
 65 70 75 80
 Ser Arg Arg Phe Trp His Cys Ala Arg Val Cys Asn Ser Val Lys Ala
 85 90 95
 Val Met Pro Cys Leu Ile Cys Cys Asn Trp Pro Ile Pro Leu Ser Thr
 100 105 110
 Ala Thr Lys Trp Arg Lys Lys Leu Pro Thr Lys Arg Ala Met Ile Arg
 115 120 125
 Arg Arg Arg Trp Met Leu Phe Gly Lys Lys Ser Arg Leu Asn Ser Leu
 130 135 140
 Leu Thr Lys Ala Ala Ala Ile Gln Gln Ser Leu Leu Ile Ser Val Ala
 145 150 155 160
 Leu Pro Val Pro Ser Arg Arg Asn Ile Ile Ser Ser Val Arg Gly Trp
 165 170 175
 Arg

<210> 53
 <211> 552
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (3)...(552)
 <223> Synthetically generated nucleic acid

<400> 53
 ga tcc gct cga tgc cca ggc cca gta cag cga act gtt cgc cca tgg 47
 Ser Ala Arg Cys Pro Gly Pro Val Gln Arg Thr Val Arg Pro Trp
 1 5 10 15
 ccg cgc cac gtc act gtt gct att cga aca tgt tca cgg tga atc ccg 95
 Pro Arg His Val Thr Val Ala Ile Arg Thr Cys Ser Arg * Ile Pro
 20 25 30
 tga ccg cgg cca ggc gat ggt gga cct gct ggc gca gta cga gca gca 143
 * Pro Arg Pro Gly Asp Gly Gly Pro Ala Gly Ala Val Arg Ala Ala

35	40	45	
cgg ttt gca gtt aaa cag ccg cga att acc gga cca cct gcc gct gta			191
Arg Phe Ala Val Lys Gln Pro Arg Ile Thr Gly Pro Pro Ala Ala Val			
50	55	60	
tct gga gta cct gtc gca gct gcc gca agg cga agc cgt gga agg ttt			239
Ser Gly Val Pro Val Ala Ala Ala Ala Arg Arg Ser Arg Gly Arg Phe			
65	70	75	
gaa aga tat cgc gcc gat tct ggc att gct gag cgc gcg tct gca aca			287
Glu Arg Tyr Arg Ala Asp Ser Gly Ile Ala Glu Arg Ala Ser Ala Thr			
80	85	90	
gcg tga aag ccg tta tgc cgt gat gtt tga tct gct gct gaa att ggc			335
Ala * Lys Pro Leu Cys Arg Asp Val * Ser Ala Ala Glu Ile Gly			
95	100	105	
cga tac cgc tat cga cag cga caa agt ggc gga aaa aat tgc cga cga			383
Arg Tyr Arg Tyr Arg Gln Arg Gln Ser Gly Gly Lys Asn Cys Arg Arg			
110	115	120	
agc gcg cga tga tac gcc gca ggc gct gga tgc tgt ttg gga aga aga			431
Ser Ala Arg * Tyr Ala Ala Gly Ala Gly Cys Cys Leu Gly Arg Arg			
125	130	135	
gca ggt taa att ctt tgc tga caa agg ctg cgg cga ttc agc aat cac			479
Ala Gly * Ile Leu Cys * Gln Arg Leu Arg Arg Phe Ser Asn His			
140	145	150	
tgc tca tca gcg tcg ctt tgc cgg tgc cgt cgc gcc gca ata tct gaa			527
Cys Ser Ser Ala Ser Leu Cys Arg Cys Arg Arg Ala Ala Ile Ser Glu			
155	160	165	
tat cct cgg tga gag gct gga gag t			552
Tyr Pro Arg * Glu Ala Gly Glu			
170	175		

<210> 54

<211> 175

<212> PRT

<213> Homosapiens

<220>

<223> Frame shift sequence

<400> 54

Ser Ala Arg Cys Pro Gly Pro Val Gln Arg Thr Val Arg Pro Trp Pro			
1	5	10	15
Arg His Val Thr Val Ala Ile Arg Thr Cys Ser Arg Ile Pro Pro Arg			
20	25	30	
Pro Gly Asp Gly Gly Pro Ala Gly Ala Val Arg Ala Ala Arg Phe Ala			
35	40	45	
Val Lys Gln Pro Arg Ile Thr Gly Pro Pro Ala Ala Val Ser Gly Val			
50	55	60	
Pro Val Ala Ala Ala Ala Arg Arg Ser Arg Gly Arg Phe Glu Arg Tyr			
65	70	75	80
Arg Ala Asp Ser Gly Ile Ala Glu Arg Ala Ser Ala Thr Ala Lys Pro			
85	90	95	
Leu Cys Arg Asp Val Ser Ala Ala Glu Ile Gly Arg Tyr Arg Tyr Arg			

	100		105		110
Gln Arg Gln Ser Gly Gly Lys Asn Cys Arg Arg Ser Ala Arg Tyr Ala					
115		120		125	
Ala Gly Ala Gly Cys Cys Leu Gly Arg Arg Ala Gly Ile Leu Cys Gln					
130		135		140	
Arg Leu Arg Arg Phe Ser Asn His Cys Ser Ser Ala Ser Leu Cys Arg					
145		150		155	160
Cys Arg Arg Ala Ala Ile Ser Glu Tyr Pro Arg Glu Ala Gly Glu					
	165		170		175

<210> 55
 <211> 554
 <212> DNA
 <213> Homosapiens

<220>
 <223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 55	
actctccagc ctctcaccga ggatattcag atattgcggc ggcagggcac cggcaaagcg	60
acgctgatga gcagtgattg ctgaatcgcc gcagcctttg tcagcaaaga atttaacctg	120
ctcttcttcc caaacagcat ccagcgctg cggcgatatca tcgcgcgctt cgtcggcaat	180
tttttcggcc actttgtcgc tgtcgatagc aggttatcgg ccaatttcag cagcagatca	240
aacatcacgg cataacggct ttcacgctgt tgcagacgcg cgctcagcaa tgccagaatc	300
ggcgcgatat ctttcaaacc ttccacggct tcgccttgcg gcagctgcga caggtactcc	360
agatatcagc ggcaggtggc cggtaattcg cggctgttta actgcaaacc gtgctgctcg	420
tactgcgcca gcaggtccac catcgcttgg ccgcggtcac gggattcacc gtgaacatgt	480
tcgaatagca acagtgacgt ggcgcggcca tgggcgaaca gttcgctgta ctgggcctgg	540
gcacgagcg gatc	554

<210> 56
 <211> 179
 <212> PRT
 <213> Homosapiens

<220>
 <223> Frame shift sequence

<223> Reverse strand

<400> 56	
Thr Leu Gln Pro Leu Thr Glu Asp Ile Gln Ile Leu Arg Arg Asp Gly	
1	15
Thr Gly Lys Ala Thr Leu Met Ser Ser Asp Cys Ile Ala Ala Ala Phe	
20	30
Val Ser Lys Glu Phe Asn Leu Leu Phe Phe Pro Asn Ser Ile Gln Arg	
35	45
Leu Arg Arg Ile Ile Ala Arg Phe Val Gly Asn Phe Phe Arg His Phe	
50	60
Val Ala Val Asp Ser Gly Ile Gly Gln Phe Gln Gln Ile Lys His	
65	80
His Gly Ile Thr Ala Phe Thr Leu Leu Gln Thr Arg Ala Gln Gln Cys	
85	95
Gln Asn Arg Arg Asp Ile Phe Gln Arg Phe His Gly Phe Ala Leu Arg	
100	110
Gln Leu Arg Gln Val Leu Gln Ile Gln Arg Gln Val Val Arg Arg Ala	
115	125
Ala Val Leu Gln Thr Val Leu Val Leu Arg Gln Val His His	
130	140

Arg Leu Ala Ala Val Thr Gly Phe Thr Val Asn Met Phe Glu Gln Gln
 145 150 155 160
 Arg Gly Ala Ala Met Gly Glu Gln Phe Ala Val Leu Gly Leu Gly Ile
 165 170 175
 Glu Arg Ile

<210> 57
 <211> 179
 <212> PRT
 <213> Homosapiens

<220>
 <223> Frame shift sequence

<223> Reverse strand

<400> 57
 Leu Ser Ser Leu Ser Pro Arg Ile Phe Arg Tyr Cys Gly Ala Thr Ala
 1 5 10 15
 Pro Ala Lys Arg Arg Ala Val Ile Ala Glu Ser Pro Gln Pro Leu Ser
 20 25 30
 Ala Lys Asn Leu Thr Cys Ser Ser Gln Thr Ala Ser Ser Ala Cys
 35 40 45
 Gly Val Ser Ser Arg Ala Ser Ser Ala Ile Phe Ser Ala Thr Leu Ser
 50 55 60
 Leu Ser Ile Ala Val Ser Ala Asn Phe Ser Ser Arg Ser Asn Ile Thr
 65 70 75 80
 Ala Arg Leu Ser Arg Cys Cys Arg Arg Ala Leu Ser Asn Ala Arg Ile
 85 90 95
 Gly Ala Ile Ser Phe Lys Pro Ser Thr Ala Ser Pro Cys Gly Ser Cys
 100 105 110
 Asp Arg Tyr Ser Arg Tyr Ser Gly Arg Trp Ser Gly Asn Ser Arg Leu
 115 120 125
 Phe Asn Cys Lys Pro Cys Cys Ser Tyr Cys Ala Ser Arg Ser Thr Ile
 130 135 140
 Ala Trp Pro Arg Ser Arg Asp Ser Pro Thr Cys Ser Asn Ser Asn Ser
 145 150 155 160
 Asp Val Ala Arg Pro Trp Ala Asn Ser Ser Leu Tyr Trp Ala Trp Ala
 165 170 175
 Ser Ser Gly

<210> 58
 <211> 180
 <212> PRT
 <213> Homosapiens

<220>
 <223> Frame shift sequence

<223> Reverse strand

<400> 58
 Ser Pro Ala Ser His Arg Gly Tyr Ser Asp Ile Ala Ala Arg Arg His
 1 5 10 15
 Arg Gln Ser Asp Ala Asp Glu Gln Leu Leu Asn Arg Arg Ser Leu Cys
 20 25 30
 Gln Gln Arg Ile Pro Ala Leu Leu Pro Lys Gln His Pro Ala Pro Ala
 35 40 45
 Ala Tyr His Arg Ala Leu Arg Arg Gln Phe Phe Pro Pro Leu Cys Arg

50		55		60	
Cys Arg Arg Tyr Arg	Pro Ile Ser Ala Ala	Asp Gln Thr Ser Arg His			
65	70	75	80		
Asn Gly Phe His Ala	Val Ala Asp Ala Arg	Ser Ala Met Pro Glu Ser			
	85	90	95		
Ala Arg Tyr Leu Ser	Asn Leu Pro Arg Leu	Arg Leu Ala Ala Ala			
	100	105	110		
Thr Gly Thr Pro Asp	Thr Ala Ala Gly Gly	Pro Val Ile Arg Gly Cys			
	115	120	125		
Leu Arg Ala Asn Arg	Ala Ala Arg Thr Ala	Pro Ala Gly Pro Pro Ser			
	130	135	140		
Pro Gly Arg Gly His	Gly Ile His Arg Glu	His Val Arg Ile Ala Thr			
145	150	155	160		
Val Thr Trp Arg Gly	His Gly Arg Thr Val	Arg Cys Thr Gly Pro Gly			
	165	170	175		
His Arg Ala Asp					
	180				

<210> 59

<211> 265

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (1)...(265)

<223> N= A,T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 59

gat cct nac aca nta gcc cgt gga cgc att tgc gtc gac cct cat ang	48
Asp Pro Xaa Thr Xaa Ala Arg Gly Arg Ile Cys Val Asp Pro His Xaa	
1 5 10 15	

gaa gcg ata cga ggc ggg tna aag tga aca tcc gcc gag cac ggc agc	96
Glu Ala Ile Arg Gly Gly Xaa Lys * Thr Ser Ala Glu His Gly Ser	
20 25 30	

gac gcc tcc gct cac cgt cng cgc agt act tcc tcg ggt cgc cgc gcc	144
Asp Ala Ser Ala His Arg Xaa Arg Ser Thr Ser Ser Gly Arg Arg Ala	
35 40 45	

tag cac tct gcg ccg tga cat caa ncc gtg aac cca cgg gag act ttg	192
* His Ser Ala Pro * His Gln Xaa Val Asn Pro Arg Glu Thr Leu	
50 55 60	

cgc cgc naa ggg atg agt cca cta tta gat gac gca tgg cta cga gcc	240
Arg Arg Xaa Gly Met Ser Pro Leu Leu Asp Asp Ala Trp Leu Arg Ala	
65 70 75	

nat cct cgg tga naa gct gga gag t	265
Xaa Pro Arg * Xaa Ala Gly Glu	
80	

<210> 60

<211> 84

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 60

```

Asp Pro Xaa Thr Xaa Ala Arg Gly Arg Ile Cys Val Asp Pro His Xaa
 1           5           10           15
Glu Ala Ile Arg Gly Gly Xaa Lys Thr Ser Ala Glu His Gly Ser Asp
          20          25          30
Ala Ser Ala His Arg Xaa Arg Ser Ser Gly Arg Arg Ala His
          35          40          45
Ser Ala Pro His Gln Xaa Val Asn Pro Arg Glu Thr Leu Arg Arg Xaa
          50          55          60
Gly Met Ser Pro Leu Leu Asp Asp Ala Trp Leu Arg Ala Xaa Pro Arg
65          70          75          80
Xaa Ala Gly Glu

```

<210> 61

<211> 265

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (2)...(265)

<223> N= A,T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 61

```

g atc ctn aca can tag ccc gtg gac gca ttt gcg tgc acc ctc ata ngg      49
  Ile Leu Thr Xaa *  Pro Val Asp Ala Phe Ala Ser Thr Leu Ile Xaa
    1           5           10           15

aag cga tac gag gcg ggt naa agt gaa cat ccg ccg agc acg gca gcg      97
  Lys Arg Tyr Glu Ala Gly Xaa Ser Glu His Pro Pro Ser Thr Ala Ala
          20          25          30

acg cct ccg ctc acc gtc ngc gca gta ctt cct cgg gtc gcc gcg cct      145
  Thr Pro Pro Leu Thr Val Xaa Ala Val Leu Pro Arg Val Ala Ala Pro
          35          40          45

agc act ctg cgc cgt gac atc aan ccg tga acc cac ggg aga ctt tgc      193
  Ser Thr Leu Arg Arg Asp Ile Xaa Pro *  Thr His Gly Arg Leu Cys
          50          55          60

gcc gcn aag gga tga gtc cac tat tag atg acg cat ggc tac gag ccn      241
  Ala Ala Lys Gly *  Val His Tyr *  Met Thr His Gly Tyr Glu Pro
          65          70          75

atc ctc ggt gan aag ctg gag agt      265
  Ile Leu Gly Xaa Lys Leu Glu Ser
          80

```

<210> 62

<211> 84

<210> 64
 <211> 86
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa=any amino acid

<223> Frame shift sequence

<400> 64
 Ser Xaa His Xaa Ser Pro Trp Thr His Leu Arg Arg Pro Ser Xaa Gly
 1 5 10 15
 Ser Asp Thr Arg Arg Val Lys Val Asn Ile Arg Arg Ala Arg Gln Arg
 20 25 30
 Arg Leu Arg Ser Pro Ser Ala Gln Tyr Phe Leu Gly Ser Pro Arg Leu
 35 40 45
 Ala Leu Cys Ala Val Thr Ser Xaa Arg Glu Pro Thr Gly Asp Phe Ala
 50 55 60
 Pro Xaa Arg Asp Glu Ser Thr Ile Arg Arg Met Ala Thr Ser Xaa Ser
 65 70 75 80
 Ser Val Xaa Ser Trp Arg
 85

<210> 65
 <211> 265
 <212> DNA
 <213> Homosapiens

<220>
 <223> N= A, T, C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 65
 actctccagc ttntcaccga ggatnggctc gtagccatgc gtcattctaat agtggactca 60
 tcccttngcg gcgcaaagtc tcccgtgggt tcacggnttg atgtcacggc gcagagtgc 120
 aggcgcggcg acccgaggaa gtactgcgcn gacggtgagc ggaggcgteg ctgccgtgct 180
 cggcggatgt tcaatttnac ccgcctcgta tcgcttcctt atgagggtcg acgcaaatgc 240
 gtccacgggc tantgtgtna ggatc 265

<210> 66
 <211> 88
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 66
 Thr Leu Gln Leu Xaa Thr Glu Asp Xaa Leu Val Ala Met Arg His Leu
 1 5 10 15
 Ile Val Asp Ser Ser Leu Xaa Gly Ala Lys Ser Pro Val Gly Ser Arg
 20 25 30

Xaa Asp Val Thr Ala Gln Ser Ala Arg Arg Gly Asp Pro Arg Lys Tyr
 35 40 45
 Cys Xaa Asp Gly Glu Arg Arg Arg Cys Arg Ala Arg Arg Met Phe
 50 55 60
 Thr Xaa Thr Arg Leu Val Ser Leu Xaa Tyr Glu Gly Arg Arg Lys Cys
 65 70 75 80
 Val His Gly Leu Xaa Cys Xaa Asp
 85

<210> 67
 <211> 85
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 67
 Leu Ser Ser Xaa Ser Pro Arg Xaa Gly Ser Pro Cys Val Ile Trp Thr
 1 5 10 15
 His Pro Xaa Ala Ala Gln Ser Leu Pro Trp Val His Xaa Leu Met Ser
 20 25 30
 Arg Arg Arg Val Leu Gly Ala Ala Thr Arg Gly Ser Thr Ala Xaa Thr
 35 40 45
 Val Ser Gly Gly Val Ala Ala Val Leu Gly Gly Cys Ser Leu Xaa Pro
 50 55 60
 Ala Ser Tyr Arg Phe Xaa Met Arg Val Asp Ala Asn Ala Ser Thr Gly
 65 70 75 80
 Xaa Cys Xaa Arg Ile
 85

<210> 68
 <211> 83
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 68
 Ser Pro Ala Xaa His Arg Gly Xaa Ala Arg Ser His Ala Ser Ser Asn
 1 5 10 15
 Ser Gly Leu Ile Pro Xaa Arg Arg Lys Val Ser Arg Gly Phe Thr Xaa
 20 25 30
 Cys His Gly Ala Glu Cys Ala Arg Arg Pro Glu Glu Val Leu Arg Xaa
 35 40 45
 Arg Ala Glu Ala Ser Leu Pro Cys Ser Ala Asp Val His Phe Xaa Pro
 50 55 60
 Pro Arg Ile Ala Ser Xaa Gly Ser Thr Gln Met Arg Pro Arg Ala Xaa
 65 70 75 80
 Val Xaa Gly

<210> 69
 <211> 317
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (1)...(317)
 <223> N= A,T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 69
 gat ccg gcc ncg cac gan ctt acc ggt naa aac ttc cnc ncc nat aat 48
 Asp Pro Ala Xaa His Xaa Leu Thr Gly Xaa Asn Phe Xaa Xaa Xaa Asn
 1 5 10 15
 att tgc cgc gcg agc cgc cct gan gct ctc ggc gta act ccg gat gca 96
 Ile Cys Arg Ala Ser Arg Pro Xaa Ala Leu Gly Val Thr Pro Asp Ala
 20 25 30
 cgg ggg acc gtg acg gtt gta ntg ccc tgg ctt ttc tca gcn gaa atc 144
 Arg Gly Thr Val Thr Val Val Xaa Pro Trp Leu Phe Ser Ala Glu Ile
 35 40 45
 tgc aca gcc atc ttc cga tgc atc tgg cgc agg tgg ggc ggc nca aaa 192
 Cys Thr Ala Ile Phe Arg Ser Ile Trp Arg Arg Trp Gly Gly Xaa Lys
 50 55 60
 cgg tgg gca tct cca aac cgc agg aac gtg ttt tgc agg atg tgc aac 240
 Arg Trp Ala Ser Pro Asn Arg Arg Asn Val Phe Cys Arg Met Ser Asn
 65 70 75 80
 atc atc cac gct tgc gtn ccc aac ggc tac ttc gcc cgg tac cgg gcc 288
 Ile Ile His Ala Ser Val Pro Asn Gly Tyr Phe Ala Arg Tyr Arg Ala
 85 90 95
 atg tca tcc tgc gtg ana agc tgg ana nt 317
 Met Ser Ser Ser Val Xaa Ser Trp Xaa
 100 105

<210> 70
 <211> 105
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 70
 Asp Pro Ala Xaa His Xaa Leu Thr Gly Xaa Asn Phe Xaa Xaa Xaa Asn
 1 5 10 15
 Ile Cys Arg Ala Ser Arg Pro Xaa Ala Leu Gly Val Thr Pro Asp Ala
 20 25 30
 Arg Gly Thr Val Thr Val Val Xaa Pro Trp Leu Phe Ser Ala Glu Ile
 35 40 45
 Cys Thr Ala Ile Phe Arg Ser Ile Trp Arg Arg Trp Gly Gly Xaa Lys

```

      50              55              60
Arg Trp Ala Ser Pro Asn Arg Arg Asn Val Phe Cys Arg Met Ser Asn
65              70              75              80
Ile Ile His Ala Ser Val Pro Asn Gly Tyr Phe Ala Arg Tyr Arg Ala
      85              90              95
Met Ser Ser Ser Val Xaa Ser Trp Xaa
      100              105

```

<210> 71
 <211> 317
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (2)...(317)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

```

<400> 71
g atc cgg ccn cgc acg anc tta ccg gtn aaa act tcc ncn ccn ata ata      49
  Ile Arg Pro Arg Thr Xaa Leu Pro Val Lys Thr Ser Xaa Pro Ile Ile
    1              5              10              15

ttt gcc gcg cga gcc gcc ctg ang ctc tgc gcg taa ctc cgg atg cac      97
Phe Ala Ala Arg Ala Ala Leu Xaa Leu Ser Ala * Leu Arg Met His
      20              25              30

ggg gga ccg tga cgg ttg tan tgc cct ggc ttt tct cag cng aaa tct      145
Gly Gly Pro * Arg Leu Xaa Cys Pro Gly Phe Ser Gln Xaa Lys Ser
      35              40              45

gca cag cca tct tcc gat cga tct ggc gca ggt ggg gcg gcn caa aac      193
Ala Gln Pro Ser Ser Asp Arg Ser Gly Ala Gly Gly Ala Ala Gln Asn
      50              55              60

ggt ggg cat ctc caa acc gca gga acg tgt ttt gca gga tgt cga aca      241
Gly Gly His Leu Gln Thr Ala Gly Thr Cys Phe Ala Gly Cys Arg Thr
      65              70              75

tca tcc acg ctt cgg tnc cca acg gct act tgc ccc ggt acc ggg cca      289
Ser Ser Thr Leu Arg Xaa Pro Thr Ala Thr Ser Pro Gly Thr Gly Pro
      80              85              90

tgt cat cct cgg tga naa gct gga nan t      317
Cys His Pro Arg * Xaa Ala Gly Xaa
      95              100

```

<210> 72
 <211> 102
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence

<400> 72

```

Ile Arg Pro Arg Thr Xaa Leu Pro Val Lys Thr Ser Xaa Pro Ile Ile
1           5           10           15
Phe Ala Ala Arg Ala Ala Leu Xaa Leu Ser Ala Leu Arg Met His Gly
20           25           30
Gly Pro Arg Leu Xaa Cys Pro Gly Phe Ser Gln Xaa Lys Ser Ala Gln
35           40           45
Pro Ser Ser Asp Arg Ser Gly Ala Gly Gly Ala Ala Gln Asn Gly Gly
50           55           60
His Leu Gln Thr Ala Gly Thr Cys Phe Ala Gly Cys Arg Thr Ser Ser
65           70           75           80
Thr Leu Arg Xaa Pro Thr Ala Thr Ser Pro Gly Thr Gly Pro Cys His
85           90           95
Pro Arg Xaa Ala Gly Xaa
100

```

<210> 73

<211> 317

<212> DNA

<213> Homosapiens

<220>

<221> CDS

<222> (3)...(317)

<223> N= A, T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 73

```

ga tcc ggc cnc gca cga nct tac cgg tna aaa ctt ccn cnc cna taa      47
  Ser Gly Xaa Ala Arg Xaa Tyr Arg Xaa Lys Leu Pro Xaa Xaa *
    1           5           10

tat ttg ccg cgc gag ccg ccc tga ngc tct cgg cgt aac tcc gga tgc      95
Tyr Leu Pro Arg Glu Pro Pro * Xaa Ser Arg Arg Asn Ser Gly Cys
  15           20           25

acg ggg gac cgt gac ggt tgt ant gcc ctg gct ttt ctc agc nga aat      143
Thr Gly Asp Arg Asp Gly Cys Xaa Ala Leu Ala Phe Leu Ser Xaa Asn
  30           35           40           45

ctg cac agc cat ctt ccg atc gat ctg gcg cag gtg ggg cgg cnc aaa      191
Leu His Ser His Leu Pro Ile Asp Leu Ala Gln Val Gly Arg Xaa Lys
           50           55           60

acg gtg ggc atc tcc aaa ccg cag gaa cgt gtt ttg cag gat gtc gaa      239
Thr Val Gly Ile Ser Lys Pro Gln Glu Arg Val Leu Gln Asp Val Glu
           65           70           75

cat cat cca cgc ttc ggt ncc caa cgg cta ctt cgc ccg gta ccg ggc      287
His His Pro Arg Phe Gly Xaa Gln Arg Leu Leu Arg Pro Val Pro Gly
           80           85           90

cat gtc atc ctc ggt gan aag ctg gan ant      317
His Val Ile Leu Gly Xaa Lys Leu Xaa Xaa
  95           100

```

<210> 74

<211> 103

<212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 74
 Ser Gly Xaa Ala Arg Xaa Tyr Arg Xaa Lys Leu Pro Xaa Xaa Tyr Leu
 1 5 10 15
 Pro Arg Glu Pro Pro Xaa Ser Arg Arg Asn Ser Gly Cys Thr Gly Asp
 20 25 30
 Arg Asp Gly Cys Xaa Ala Leu Ala Phe Leu Ser Xaa Asn Leu His Ser
 35 40 45
 His Leu Pro Ile Asp Leu Ala Gln Val Gly Arg Xaa Lys Thr Val Gly
 50 55 60
 Ile Ser Lys Pro Gln Glu Arg Val Leu Gln Asp Val Glu His His Pro
 65 70 75 80
 Arg Phe Gly Xaa Gln Arg Leu Leu Arg Pro Val Pro Gly His Val Ile
 85 90 95
 Leu Gly Xaa Lys Leu Xaa Xaa
 100

<210> 75
 <211> 316
 <212> DNA
 <213> Homosapiens

<220>
 <223> N= A, T, C or G

<223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 75
 antntccagc ttntcaccga ggatgacatg gcccggtacc gggcgaagta gccgttgggn 60
 accgaagcgt ggatgatgtt cgacatcctg caaaacacgt tcctgcgggt tggagatgcc 120
 caccgttttg ngccgcccac ctgcgccaga tcgatcggaa gatggctgtg cagatttcng 180
 ctgagaaaaag ccagggcant acaaccgtca cggcccccg tgcacccgga gttacgccga 240
 gagntcagg gcggctcgcg cggcaaatat tatnggngng gaagttttna ccggttaagnt 300
 cgtgcgnggc cggatc 316

<210> 76
 <211> 104
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 76
 Xaa Xaa Gln Leu Xaa Thr Glu Asp Asp Met Ala Arg Tyr Arg Ala Lys
 1 5 10 15
 Pro Leu Xaa Thr Glu Ala Trp Met Met Phe Asp Ile Leu Gln Asn Thr
 20 25 30

Phe Leu Arg Phe Gly Asp Ala His Arg Phe Xaa Pro Pro His Leu Arg
 35 40 45
 Gln Ile Asp Arg Lys Met Ala Val Gln Ile Xaa Ala Glu Lys Ser Gln
 50 55 60
 Gly Xaa Thr Thr Val Thr Val Pro Arg Ala Ser Gly Val Thr Pro Arg
 65 70 75 80
 Xaa Ser Gly Arg Leu Ala Arg Gln Ile Leu Xaa Xaa Xaa Lys Phe Xaa
 85 90 95
 Pro Val Xaa Ser Cys Xaa Ala Gly
 100

<210> 77
 <211> 103
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 77
 Xaa Ser Ser Xaa Ser Pro Arg Met Thr Trp Pro Gly Thr Gly Arg Ser
 1 5 10 15
 Ser Arg Trp Xaa Pro Lys Arg Gly Cys Ser Thr Ser Cys Lys Thr Arg
 20 25 30
 Ser Cys Gly Leu Arg Met Pro Thr Val Leu Xaa Arg Pro Thr Cys Ala
 35 40 45
 Arg Ser Ile Gly Arg Trp Leu Cys Arg Phe Xaa Leu Arg Lys Ala Arg
 50 55 60
 Ala Xaa Gln Pro Ser Arg Ser Pro Val His Pro Glu Leu Arg Arg Glu
 65 70 75 80
 Xaa Gln Gly Gly Ser Arg Gly Lys Tyr Tyr Xaa Xaa Gly Ser Phe Xaa
 85 90 95
 Arg Xaa Arg Ala Xaa Pro Asp
 100

<210> 78
 <211> 103
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 78
 Xaa Pro Ala Xaa His Arg Gly His Gly Pro Val Pro Gly Glu Val Ala
 1 5 10 15
 Val Gly Xaa Arg Ser Val Asp Asp Val Arg His Pro Ala Lys His Val
 20 25 30
 Pro Ala Val Trp Arg Cys Pro Pro Phe Xaa Ala Ala Pro Pro Ala Pro
 35 40 45
 Asp Arg Ser Glu Asp Gly Cys Ala Asp Phe Xaa Glu Lys Pro Gly Xaa
 50 55 60
 Tyr Asn Arg His Gly Pro Pro Cys Ile Arg Ser Tyr Ala Glu Ser Xaa

```

65          70          75          80
Arg Ala Ala Arg Ala Ala Asn Ile Xaa Xaa Xaa Glu Val Xaa Thr Gly
          85          90          95
Lys Xaa Val Xaa Gly Arg Ile
          100

```

<210> 79
 <211> 341
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (1)...(341)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

```

<400> 79
act ctc cag cct cgc acc gag gat cag ggc gtc gtc gac tcc gtc gac      48
Thr Leu Gln Pro Arg Thr Glu Asp Gln Gly Val Val Asp Ser Val Asp
  1          5          10          15

ctg acc gcc tcc ccn ccg ctg ctc tcg atc ggc ggc cag acc tac acc      96
Leu Thr Ala Ser Pro Pro Leu Leu Ser Ile Gly Gly Gln Thr Tyr Thr
          20          25          30

anc gac gta gat caa gcg cgt ggt gcg cgg cgc nac nag can can cta      144
Xaa Asp Val Asp Gln Ala Arg Gly Ala Arg Arg Xaa Xaa Xaa Xaa Leu
          35          40          45

ant caa ggc ctc gct gca tcc cgc caa tcc agc gct cag ctt cgc ggg      192
Xaa Gln Gly Leu Ala Ala Ser Arg Gln Ser Ser Ala Gln Leu Arg Gly
          50          55          60

aat tgc gcg anc gct ttt gcg cgt cnc gag tna ccg cat aca cac ctg      240
Asn Cys Ala Xaa Ala Phe Ala Arg Xaa Glu Xaa Pro His Thr His Leu
          65          70          75          80

ccg tcc ctg cga aag caa gga ccc ata ctc cgc ngc ggg tgt tgt tga      288
Pro Ser Leu Arg Lys Gln Gly Pro Ile Leu Arg Xaa Gly Cys Cys *
          85          90          95

cgg gac tcg tca tgg cgg caa cgc aca acg tnn aac ttc tgt ggt tat      336
Arg Asp Ser Ser Trp Arg Gln Arg Thr Thr Xaa Asn Phe Cys Gly Tyr
          100          105          110

gga tc      341
Gly

```

<210> 80
 <211> 112
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<400> 80

<210> 81

$\langle 211 \rangle$ 341

<212> DNA

<213> Homosapiens

<220>

<221> CDS

 $\langle 222 \rangle \quad (2) \dots (341)$

<223> N= A, T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 81

a ctc tcc agc ctc gca ccg agg atc agg gcg tcg tcg act ccg tcg acc 49
Leu Ser Ser Leu Ala Pro Arg Ile Arg Ala Ser Ser Thr Pro Ser Thr
1 5 10 15

tga ccg cct ccc cnc cgc tgc tct cga tcg gcg gcc aga cct aca cca 97
 * Pro Pro Pro Xaa Arg Cys Ser Arg Ser Ala Ala Arg Pro Thr Pro
 20 25 30

ncg acg tag atc aag cgc gtg gtg cgc ggc gcn acn agc anc anc taa 145
 Xaa Thr * Ile Lys Arg Val Val Arg Gly Ala Thr Ser Xaa Xaa *
 35 40 45

ntc aag gcc tcg ctg cat ccc gcc aat cca gcg ctc agc ttc gcg gga 193
Xaa Lys Ala Ser Leu His Pro Ala Asn Pro Ala Leu Ser Phe Ala Gly
50 55 60

att gcg cga ncg ctt ttg cgc gtc ncg agt nac cgc ata cac acc tgc 241
Ile Ala Arg Xaa Leu Leu Arg Val Xaa Ser Xaa Arg Ile His Thr Cys
65 70 75

cgt ccc tgc gaa agc aag gac cca tac tcc gcg gcg ggt gtt gtt gac 289
 Arg Pro Cys Glu Ser Lys Asp Pro Tyr Ser Ala Ala Gly Val Val Asp
 80 85 90

ggg act cgt cat ggc ggc aac gca caa cgt nna act tct gtg gtt atg 337
Gly Thr Arg His Gly Gly Asn Ala Gln Arg Xaa Thr Ser Val Val Met
95 100 105

gat c 341

Asp
110

<210> 82
<211> 110
<212> PRT
<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<400> 82

Leu	Ser	Ser	Leu	Ala	Pro	Arg	Ile	Arg	Ala	Ser	Ser	Thr	Pro	Ser	Thr
1			5					10					15		
Pro	Pro	Pro	Xaa	Arg	Cys	Ser	Arg	Ser	Ala	Ala	Arg	Pro	Thr	Pro	Xaa
		20					25					30			
Thr	Ile	Lys	Arg	Val	Val	Arg	Gly	Ala	Thr	Ser	Xaa	Xaa	Xaa	Lys	Ala
	35					40					45				
Ser	Leu	His	Pro	Ala	Asn	Pro	Ala	Leu	Ser	Phe	Ala	Gly	Ile	Ala	Arg
	50				55				60						
Xaa	Leu	Leu	Arg	Val	Xaa	Ser	Xaa	Arg	Ile	His	Thr	Cys	Arg	Pro	Cys
65			70					75						80	
Glu	Ser	Lys	Asp	Pro	Tyr	Ser	Ala	Ala	Gly	Val	Val	Asp	Gly	Thr	Arg
			85					90					95		
His	Gly	Gly	Asn	Ala	Gln	Arg	Xaa	Thr	Ser	Val	Val	Met	Asp		
		100					105						110		

<210> 83
<211> 341
<212> DNA
<213> Homosapiens

<220>

<221> CDS

<222> (3)...(341)

<223> N= A, T, C or G

Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 83

ac	tct	cca	gcc	tgc	cac	cga	gga	tca	ggg	cg	cg	cga	ctc	cg	cga	47
	Ser	Pro	Ala	Ser	His	Arg	Gly	Ser	Gly	Arg	Arg	Arg	Leu	Arg	Arg	
1				5					10					15		
cct	gac	cgc	ctc	ccc	ncc	gct	gct	ctc	gat	cgg	cgg	cca	gac	cta	cac	95
Pro	Asp	Arg	Leu	Pro	Xaa	Ala	Ala	Leu	Asp	Arg	Arg	Pro	Asp	Leu	His	
			20					25					30			
can	cga	cg	aga	tca	agc	gcg	tgg	tgc	gcg	gcg	cna	cna	gca	nca	nct	143
Xaa	Arg	Arg	Arg	Ser	Ser	Ala	Trp	Cys	Ala	Ala	Xaa	Xaa	Ala	Xaa	Xaa	
			35				40						45			
aan	tca	agg	cct	cgc	tgc	atc	ccg	cca	atc	cag	cgc	tca	gct	tgc	cgg	191
Xaa	Ser	Arg	Pro	Arg	Cys	Ile	Pro	Pro	Ile	Gln	Arg	Ser	Ala	Ser	Arg	
			50				55					60				
gaa	ttg	cgc	gan	cgc	ttt	tgc	gcg	tcn	cga	gtn	acc	gca	tac	aca	cct	239

Glu Leu Arg Xaa Arg Phe Cys Ala Ser Arg Val Thr Ala Tyr Thr Pro
 65 70 75

gcc gtc cct gcg aaa gca agg acc cat act ccg cng cgg gtg ttg ttg 287
 Ala Val Pro Ala Lys Ala Arg Thr His Thr Pro Xaa Arg Val Leu Leu
 80 85 90 95

acg gga ctc gtc atg gcg gca acg cac aac gtn naa ctt ctg tgg tta 335
 Thr Gly Leu Val Met Ala Ala Thr His Asn Val Xaa Leu Leu Trp Leu
 100 105 110

tgg atc
 Trp Ile 341

<210> 84
 <211> 113
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence

<400> 84
 Ser Pro Ala Ser His Arg Gly Ser Gly Arg Arg Arg Leu Arg Arg Pro
 1 5 10 15
 Asp Arg Leu Pro Xaa Ala Ala Leu Asp Arg Arg Pro Asp Leu His Xaa
 20 25 30
 Arg Arg Arg Ser Ser Ala Trp Cys Ala Ala Xaa Xaa Ala Xaa Xaa Xaa
 35 40 45
 Ser Arg Pro Arg Cys Ile Pro Pro Ile Gln Arg Ser Ala Ser Arg Glu
 50 55 60
 Leu Arg Xaa Arg Phe Cys Ala Ser Arg Val Thr Ala Tyr Thr Pro Ala
 65 70 75 80
 Val Pro Ala Lys Ala Arg Thr His Thr Pro Xaa Arg Val Leu Leu Thr
 85 90 95
 Gly Leu Val Met Ala Ala Thr His Asn Val Xaa Leu Leu Trp Leu Trp
 100 105 110
 Ile

<210> 85
 <211> 342
 <212> DNA
 <213> Homosapiens

<220>
 <223> N= A, T, C or G
 <223> synthetically generated nucleic acid

<223> Reverse strand

<400> 85
 gatccataac cacagaagtt nnacgttgtg cgttgccgcc atgacgagtc ccgtcaacaa 60
 caccgcgcgc ggagtatggg tccttgcttt cgcagggacg gcaggtgtgt atgcggtnac 120
 tcgngacgcg caaaagcgnt cgcgcaattc ccgcgaagct gagcgcgtgg attggcggga 180
 tgcagcgagg ccttgantta gntgntgctn gtngcgccgc gcaccacgcg cttgatctac 240

gtcgntggtg taggtctggc cgccgatcga gaggcagcgn ggggaggcgg tcaggtcgac 300
 ggagtcgacg acgccctgat cctcggtgcg aggtggaga gt 342

<210> 86
 <211> 107
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 86
 Asp Pro Pro Gln Lys Xaa Xaa Val Val Arg Cys Arg His Asp Glu Ser
 1 5 10 15
 Arg Gln Gln His Pro Xaa Arg Ser Met Gly Pro Cys Phe Arg Arg Asp
 20 25 30
 Gly Arg Cys Val Cys Gly Xaa Ser Xaa Arg Ala Lys Ala Xaa Ala Gln
 35 40 45
 Phe Pro Arg Ser Ala Leu Asp Trp Arg Asp Ala Ala Arg Pro Xaa Xaa
 50 55 60
 Xaa Cys Xaa Xaa Arg Arg Ala Pro Arg Ala Ser Thr Ser Xaa Val Val
 65 70 75 80
 Trp Pro Pro Ile Glu Ser Ser Xaa Gly Glu Ala Val Arg Ser Thr Glu
 85 90 95
 Ser Thr Thr Pro Ser Ser Val Arg Gly Trp Arg
 100 105

<210> 87
 <211> 113
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 87
 Ile His Asn His Arg Ser Xaa Thr Leu Cys Val Ala Ala Met Thr Ser
 1 5 10 15
 Pro Val Asn Asn Thr Arg Xaa Gly Val Trp Val Leu Ala Phe Ala Gly
 20 25 30
 Arg Ala Gly Val Tyr Ala Xaa Thr Xaa Asp Ala Gln Lys Xaa Ser Arg
 35 40 45
 Asn Ser Arg Glu Ala Glu Arg Trp Ile Gly Gly Met Gln Arg Gly Leu
 50 55 60
 Xaa Leu Xaa Xaa Ala Xaa Xaa Ala Ala His His Ala Leu Asp Leu Arg
 65 70 75 80
 Xaa Trp Cys Arg Ser Gly Arg Arg Ser Arg Ala Ala Xaa Gly Arg Arg
 85 90 95
 Ser Gly Arg Arg Ser Arg Arg Arg Pro Asp Pro Arg Cys Glu Ala Gly
 100 105 110
 Glu

<210> 88
 <211> 111
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence
 <223> Reverse strand

<400> 88
 Ser Ile Thr Thr Glu Val Xaa Arg Cys Ala Leu Pro Pro Arg Val Pro
 1 5 10 15
 Ser Thr Thr Pro Xaa Ala Glu Tyr Gly Ser Leu Leu Ser Gln Gly Arg
 20 25 30
 Gln Val Cys Met Arg Xaa Leu Xaa Thr Arg Lys Ser Xaa Arg Ala Ile
 35 40 45
 Pro Ala Lys Leu Ser Ala Gly Leu Ala Gly Cys Ser Glu Ala Leu Xaa
 50 55 60
 Xaa Xaa Xaa Xaa Ala Pro Arg Thr Thr Arg Leu Ile Tyr Val Xaa Gly
 65 70 75 80
 Val Gly Leu Ala Ala Asp Arg Glu Gln Arg Xaa Gly Gly Gly Gln Val
 85 90 95
 Asp Gly Val Asp Asp Ala Leu Ile Leu Gly Ala Arg Leu Glu Ser
 100 105 110

<210> 89
 <211> 256
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (1)...(256)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 89
 gat ccg cgc atc ctc tct gtg gct ctc gcg ggg tca gag gtg gat aag 48
 Asp Pro Arg Ile Leu Ser Val Ala Leu Ala Gly Ser Glu Val Asp Lys
 1 5 10 15
 gcc ggc cgc aag ctc gga ctt ccc gtc nca atc naa ggc ttc tgc gat 96
 Ala Gly Arg Lys Leu Gly Leu Pro Val Xaa Ile Xaa Gly Phe Cys Asp
 20 25 30
 cnc can tac aac tac nac ggc aat ctn aca tca cgc aag atc gca ngc 144
 Xaa Xaa Tyr Asn Tyr Xaa Gly Asn Leu Thr Ser Arg Lys Ile Ala Xaa
 35 40 45
 tcn gtc atc aag gac gcn gcg gtc ncc ncc cgg cag gtg ctc nat atn 192
 Ser Val Ile Lys Asp Ala Ala Val Xaa Xaa Arg Gln Val Leu Xaa Xaa
 50 55 60
 gtg ttg aan aac acc atc gct cct gca acg gca aga aga tca cat gca 240
 Val Leu Xaa Asn Thr Ile Ala Pro Ala Thr Ala Arg Arg Ser His Ala
 65 70 75 80

agg tcc act cgc tgt g
 Arg Ser Thr Arg Cys
 85

<210> 90
 <211> 85
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 90
 Asp Pro Arg Ile Leu Ser Val Ala Leu Ala Gly Ser Glu Val Asp Lys
 1 5 10 15
 Ala Gly Arg Lys Leu Gly Leu Pro Val Xaa Ile Xaa Gly Phe Cys Asp
 20 25 30
 Xaa Xaa Tyr Asn Tyr Xaa Gly Asn Leu Thr Ser Arg Lys Ile Ala Xaa
 35 40 45
 Ser Val Ile Lys Asp Ala Ala Val Xaa Xaa Arg Gln Val Leu Xaa Xaa
 50 55 60
 Val Leu Xaa Asn Thr Ile Ala Pro Ala Thr Ala Arg Arg Ser His Ala
 65 70 75 80
 Arg Ser Thr Arg Cys
 85

<210> 91
 <211> 256
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (2)...(256)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 91
 g atc cgc gca tcc tct ctg tgg ctc tcg cgg ggt cag agg tgg ata agg 49
 Ile Arg Ala Ser Ser Leu Trp Leu Ser Arg Gly Gln Arg Trp Ile Arg
 1 5 10 15
 ccg gcc gca agc tcg gac ttc ccg tcn caa tcn aag gct tct gcg atc 97
 Pro Ala Ala Ser Ser Asp Phe Pro Ser Gln Ser Lys Ala Ser Ala Ile
 20 25 30
 ncc ant aca act acn acg gca atc tna cat cac gca aga tcg can gct 145
 Xaa Xaa Thr Thr Thr Ala Ile Xaa His His Ala Arg Ser Xaa Ala
 35 40 45
 cng tca tca agg acg cng cgg tcn ccn ccc ggc agg tgc tcn ata tng 193
 Xaa Ser Ser Arg Thr Xaa Arg Ser Pro Pro Gly Arg Cys Ser Ile Xaa
 50 55 60
 tgt tga ana aca cca tcg ctc ctg caa cgg caa gaa gat cac atg caa 241

Cys * Xaa Thr Pro Ser Leu Leu Gln Arg Gln Glu Asp His Met Gln
 65 70 75

ggt cca ctc gct gtg
 Gly Pro Leu Ala Val
 80

256

<210> 92
 <211> 84
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<400> 92
 Ile Arg Ala Ser Ser Leu Trp Leu Ser Arg Gly Gln Arg Trp Ile Arg
 1 5 10 15
 Pro Ala Ala Ser Ser Asp Phe Pro Ser Gln Ser Lys Ala Ser Ala Ile
 20 25 30
 Xaa Xaa Thr Thr Thr Thr Ala Ile Xaa His His Ala Arg Ser Xaa Ala
 35 40 45
 Xaa Ser Ser Arg Thr Xaa Arg Ser Pro Pro Gly Arg Cys Ser Ile Xaa
 50 55 60
 Cys Xaa Thr Pro Ser Leu Leu Gln Arg Gln Glu Asp His Met Gln Gly
 65 70 75 80
 Pro Leu Ala Val

<210> 93
 <211> 256
 <212> DNA
 <213> Homosapiens

<220>
 <221> CDS
 <222> (3)...(256)
 <223> N= A, T, C or G
 Xaa= any amino acid

<223> Synthetically generated nucleic acid

<400> 93
 ga tcc gcg cat cct ctc tgt ggc tct cgc ggg gtc aga ggt gga taa 47
 Ser Ala His Pro Leu Cys Gly Ser Arg Gly Val Arg Gly Gly *
 1 5 10
 ggc cgg ccg caa gct cgg act tcc cgt cnc aat cna agg ctt ctg cga 95
 Gly Arg Pro Gln Ala Arg Thr Ser Arg Xaa Asn Xaa Arg Leu Leu Arg
 15 20 25 30
 tcn cca nta caa cta cna cgg caa tct nac atc acg caa gat cgc ang 143
 Ser Pro Xaa Gln Leu Xaa Arg Gln Ser Xaa Ile Thr Gln Asp Arg Xaa
 35 40 45
 ctc ngc cat caa gga cgc ngc ggt cnc cnc ccg gca ggt gct cna tat 191
 Leu Xaa His Gln Gly Arg Xaa Gly Xaa Xaa Pro Ala Gly Ala Xaa Tyr
 50 55 60

ngt gtt gaa naa cac cat cgc tcc tgc aac ggc aag aag atc aca tgc 239
 Xaa Val Glu Xaa His His Arg Ser Cys Asn Gly Lys Lys Ile Thr Cys
 65 70 75

aag gtc cac tcg ctg tg 256
 Lys Val His Ser Leu
 80

<210> 94
 <211> 83
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid
 <223> Frame shift sequence

<400> 94
 Ser Ala His Pro Leu Cys Gly Ser Arg Gly Val Arg Gly Gly Gly Arg
 1 5 10 15
 Pro Gln Ala Arg Thr Ser Arg Xaa Asn Xaa Arg Leu Leu Arg Ser Pro
 20 25 30
 Xaa Gln Leu Xaa Arg Gln Ser Xaa Ile Thr Gln Asp Arg Xaa Leu Xaa
 35 40 45
 His Gln Gly Arg Xaa Gly Xaa Xaa Pro Ala Gly Ala Xaa Tyr Xaa Val
 50 55 60
 Glu Xaa His His Arg Ser Cys Asn Gly Lys Lys Ile Thr Cys Lys Val
 65 70 75 80
 His Ser Leu

<210> 95
 <211> 256
 <212> DNA
 <213> Homosapiens

<220>
 <223> N= A, T, C or G
 <223> Synthetically generated nucleic acid

<223> Reverse strand

<400> 95
 cacagcgagt ggaccttgca tgtgatcttc ttgccgttgc aggagcgatg gtgttntttca 60
 acacnataatn gagcacctgc cgggngggnga ccgcggcgctc cttgatgacn gagcntgcga 120
 tcttgcgatga tgtnagattg ccgtngtagt tgtantggng atcgcagaag ccttngattg 180
 ngacgggaag tccgagcttg cggccggcct tatccacctc tgaccccgcg agagccacag 240
 agaggatgcg cggatc 256

<210> 96
 <211> 83
 <212> PRT
 <213> Homosapiens

<220>
 <223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 96

His	Ser	Glu	Gln	Thr	Leu	His	Val	Ile	Phe	Leu	Pro	Leu	Gln	Glu	Arg
1				5				10					15		
Trp	Cys	Xaa	Ser	Thr	Ser	Tyr	Xaa	Ala	Pro	Ala	Gly	Xaa	Xaa	Pro	Xaa
			20				25					30			
Arg	Pro	Xaa	Ser	Xaa	Arg	Ser	Cys	Val	Met	Xaa	Asp	Cys	Arg	Xaa	Ser
			35			40					45				
Cys	Xaa	Xaa	Asp	Arg	Arg	Ser	Leu	Xaa	Leu	Xaa	Arg	Glu	Val	Arg	Ala
	50				55				60						
Cys	Gly	Arg	Pro	Tyr	Pro	Pro	Leu	Thr	Pro	Arg	Glu	Pro	Gln	Arg	Gly
65				70					75					80	
Cys	Ala	Asp													

<210> 97

<211> 82

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 97

Thr	Ala	Ser	Gly	Pro	Cys	Met	Ser	Ser	Cys	Arg	Cys	Arg	Ser	Asp	Gly
1				5					10				15		
Val	Xaa	Gln	His	Xaa	Xaa	Glu	His	Leu	Pro	Xaa	Xaa	Asp	Arg	Xaa	Val
			20				25					30			
Leu	Asp	Asp	Xaa	Xaa	Cys	Asp	Leu	Ala	Cys	Xaa	Ile	Ala	Xaa	Val	Val
			35			40					45				
Val	Xaa	Xaa	Ile	Ala	Glu	Ala	Xaa	Asp	Xaa	Asp	Gly	Lys	Ser	Glu	Leu
	50				55				60						
Ala	Ala	Gly	Leu	Ile	His	Leu	Pro	Arg	Glu	Ser	His	Arg	Glu	Asp	Ala
65				70					75					80	
Arg	Ile														

<210> 98

<211> 83

<212> PRT

<213> Homosapiens

<220>

<223> Xaa= any amino acid

<223> Frame shift sequence

<223> Reverse strand

<400> 98

Gln	Arg	Val	Asp	Leu	Ala	Cys	Asp	Leu	Leu	Ala	Val	Ala	Gly	Ala	Met
1				5				10					15		
Val	Xaa	Phe	Asn	Xaa	Ile	Xaa	Ser	Thr	Cys	Arg	Xaa	Xaa	Thr	Xaa	Ala
			20				25					30			

Ser Leu Met Xaa Glu Xaa Ala Ile Leu Arg Asp Xaa Arg Leu Pro Xaa
 35 40 45
 Leu Xaa Trp Xaa Ser Gln Lys Pro Xaa Ile Xaa Thr Gly Ser Pro Ser
 50 55 60
 Leu Arg Pro Ala Leu Ser Thr Ser Asp Pro Ala Arg Ala Thr Glu Arg
 65 70 75 80
 Met Arg Gly

B1
 Conclude